

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:43:41 ; Search time 50 Seconds  
(without alignments)  
661.732 Million cell updates/sec

Title: US-10-622-774-2  
Perfect score: 2086  
Sequence: 1 MSDSYDDRMKDHMDERAPI.....IYIEQDADSKHGTYWYHKM 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA: \*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pdp: \*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pdp: \*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pdp: \*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pdp: \*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCRTUS COMB.pdp: \*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pdp: \*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pdp: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description                         |
|------------|--------|-------------|--------|-------|-------------------------------------|
| 1          | 1821   | 87.3        | 384    | 1     | US-08-872-302-4 Sequence 4, Appli   |
| 2          | 1510   | 72.4        | 374    | 2     | US-09-059-769-4 Sequence 4, Appli   |
| 3          | 1493   | 71.6        | 374    | 2     | US-09-059-769-2 Sequence 2, Appli   |
| 4          | 1427.5 | 68.4        | 375    | 2     | US-09-161-994A-2 Sequence 2, Appli  |
| 5          | 1279   | 61.3        | 383    | 2     | US-09-638-937-15 Sequence 15, Appl  |
| 6          | 1271   | 60.9        | 383    | 2     | US-09-059-769-12 Sequence 12, Appl  |
| 7          | 1271   | 60.9        | 383    | 2     | US-09-161-994A-16 Sequence 16, Appl |
| 8          | 1234   | 59.2        | 383    | 2     | US-09-059-769-11 Sequence 11, Appl  |
| 9          | 1234   | 59.2        | 383    | 2     | US-09-161-994A-15 Sequence 15, Appl |
| 10         | 1234   | 59.2        | 383    | 2     | US-09-837-751-31 Sequence 31, Appl  |
| 11         | 1226   | 58.8        | 383    | 2     | US-09-837-751-6 Sequence 6, Appli   |
| 12         | 1224.5 | 58.7        | 382    | 1     | US-08-872-302-2 Sequence 2, Appli   |
| 13         | 1215   | 58.2        | 383    | 1     | US-08-314-596-41 Sequence 41, Appl  |
| 14         | 1215   | 58.2        | 383    | 1     | US-08-320-982-41 Sequence 41, Appl  |
| 15         | 1215   | 58.2        | 383    | 2     | US-08-819-037-41 Sequence 41, Appl  |
| 16         | 1215   | 58.2        | 383    | 2     | US-08-530-862B-6 Sequence 6, Appli  |
| 17         | 1215   | 58.2        | 383    | 2     | US-08-597-313D-6 Sequence 6, Appli  |
| 18         | 1215   | 58.2        | 383    | 2     | US-09-059-769-9 Sequence 9, Appli   |
| 19         | 1215   | 58.2        | 383    | 2     | US-09-161-994A-14 Sequence 14, Appl |
| 20         | 1215   | 58.2        | 383    | 2     | US-09-133-962A-2 Sequence 2, Appli  |
| 21         | 1215   | 58.2        | 383    | 2     | US-09-045-940-41 Sequence 41, Appl  |
| 22         | 1215   | 58.2        | 383    | 2     | US-09-763-331-4 Sequence 4, Appli   |
| 23         | 1215   | 58.2        | 383    | 2     | US-09-697-379-2 Sequence 2, Appli   |
| 24         | 1215   | 58.2        | 383    | 2     | US-10-116-212A-2 Sequence 2, Appli  |
| 25         | 1215   | 58.2        | 383    | 2     | US-09-885-189-6 Sequence 6, Appli   |
| 26         | 1215   | 58.2        | 383    | 2     | US-09-837-751-32 Sequence 32, Appl  |

ALIGNMENTS

RESULT 1  
US-08-872-302-4  
; Sequence 4, Application US/08872302  
; Patent No. 5846784  
; GENERAL INFORMATION:  
; APPLICANT: Hitz, William D  
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. duPont de Nemours and Co.  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,302  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Majarian, William R  
; REGISTRATION NUMBER: P-41,173  
; REFERENCE/DOCKET NUMBER: BB-1084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-4926  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-302-4

Query Match 87.3%; Score 1821; DB 1; Length 384;  
Best Local Similarity 84.3%; Pred. No. 1.6e-179;  
Matches 322; Conservative 29; Mismatches 27; Indels 4; Gaps 1;  
QY 1 MSDSYDDR----MKDHMDERAPIPAPPSLDLKAIPAHCFRRSAVWSSCVVQDLII 56  
Db 3 MSDSCDDHQLVKDHNINERAPVDAAPPSLDLKAIPHCFQSAIRSSCVVQDLII 62  
QY 57 TFLTYTANTYIPLPLPLVYLAWPVYWFQCSCILTLGLVWLGHECGHHAFFSEYQWIDNAV 116

Db 63 TFLYTLANSIPLPPPLPYLAWPVYFQCSSLTGLWVIGHECHHAYSEYQWVDNTV 122  
Qy 117 GFVLHSAALLTPYFMSKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYFELDNTPGRL 176  
Db 123 GFILHSPLLTPYFMSKYSHRKHANTNSLENEEVIPKAKSQLRNSYFKNFLDNTPGRI 182  
Qy 177 ILVIMLTGPPLYLLTNVSGKYDRPTHFDPDLSPIFTRERIRIQVALSDLGIVAVFYGLK 236  
Db 183 ILLIMLTGLFLYLLTNISGKYQRFANHPDPLSPISERIRIQVLSDVGLIAVIFYGLK 242  
Qy 237 FLVOTKFGWVMCMYGVPIVGLNSFIIVITLHHTHLSPPHYDSTEWNIWIKALTTIORD 296  
Db 243 FLVAKGFGWVMYGVAPVGLNFIIMITLHHTHLSPPHYDSTEWNIWIKALTTIORD 302  
Qy 297 FGLNRVFDVTHVHLHLPYIPHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAK 356  
Db 303 FGLNRVFDVTHVHLHLPYIPHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAK 362  
Qy 357 ECIYIEQDADSKHKGTYYHYKM 378  
Db 363 ECIYIEPDEDKKHGVYHYHKM 384

## RESULT 2

US-09-059-769-4  
; Sequence 4, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-059-769-4  
Query Match 72.4%; Score 1510; DB 2; Length 374;  
Best Local Similarity 70.4%; Pred. No. 2.1e-147;  
Matches 261; Conservative 50; Mismatches 56; Indels 4; Gaps 2;  
Qy 8 RMKDHDMDERAPIDPAPFSLDLKKAIPAHCFRBSAVMSWCYVVDLIITFLLYTVANTY 67  
Db 8 RTSEKSVMERVSVDVPTFSLDLKQAIPPHCFQSRVIRSSYYVQDIIAIFYFLANTY 67  
Qy 68 IPHLPPLPYLWVPYWFQCSSLTGLWVIGHECHHAFSEYQWIDNAGFVLHSAALLTP 127  
Db 68 IPNLPPLPYLWVPYWFQCSSLTGLWVIGHECHHAFSEYQWIDNAGFVLHSAALLTP 127  
Qy 128 YFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYFELDNTPGRLIILVIMLTGPP 187  
Db 128 YFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYFELDNTPGRLIILVIMLTGPP 185  
Qy 188 LYLNTVSGKYYDRPTHFDPDLSPIFTRERIRIQVALSDLGIVAVFYGLKFLVQTGFGWV 247  
Db 186 LYLNTVSGKYYDRPTHFDPDLSPIFTRERIRIQVALSDLGIVAVFYGLKFLVQTGFGWV 245  
Qy 248 MCMYGVPIVGLNSFIIVITLHHTHLSPPHYDSTEWNIWIKALTTIORDFGLNREVDV 307  
Db 246 MCMYGVPIVGLNSFIIVITLHHTHLSPPHYDSTEWNIWIKALTTIORDFGLNREVDV 305  
Qy 308 THTVHLHLPYIPHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIYIEQDADS 367  
Db 306 THTVHLHLPYIPHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIYIEQDADS 363  
Qy 368 KHGTYHYHYKM 378  
Db 364 KLKGVYHYHYKM 374  
RESULT 3  
US-09-059-769-2  
; Sequence 2, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706



Db 79 HPLSVAMPLVWFCOGSVLTGVWVIAHCGHAFSDYQWLDLDTVGLLHLSALLVFPFSWK 138  
QY 133 YSHRKHANTNSLENEEYVYIPRTQSOLATYTYEFLDNTPGRIILVIMLTGLFPPLYLTT 192  
Db 139 YSHRHHSNTGSLERDEVFPKRGSGISWSS--EYLNPPGRVLVLLVQLTLGWPPLYLMF 196  
QY 193 NVSGKKYDRFTNHPDPLSPIETERERIQVALSDLGIVAFVGLKPLVOTKPGWVMQWVG 252  
Db 197 NVSGRPYDRFACHPFKPSPIYNDRELRQIYISDAGIVAMVGLYRLVAAKGVAMVVCYIG 256  
QY 253 VPVIGLNSFIIVITVYLHHTLSSPHYSTENWIKGALTITDRDFGLNLRVFDVTHVTHV 312  
Db 257 VPLLVNGFLVLTLYLQHTQPSLPHYDSSEWDLKALATVDYDYGFLNKVLNLTIDTHV 316  
QY 313 LHLFPYIPHYHAKESBAIKPILGDYRMIORTPFFKAMWEAKECIYEQDADSKHGT 372  
Db 317 AHLFPSTPHYHAMEATKAIPILGDYQCDRTVPFKAMVREKVECIYVEADGDKKGV 376  
QY 373 YWY 375  
Db 377 FWY 379

RESULT 6  
US-09-059-769-12  
; Sequence 12, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lenman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxysenase Genes and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GreenLee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 16-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050403  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 383 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Solanum commersonii  
US-09-059-769-12  
Query Match 60.9%; Score 1271; DB 2; Length 383;  
Best Local Similarity 58.3%; Pred. No. 1.1e-122;  
Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;  
QY 16 ERAPIDPAPPSLSDLKKAIPAHCFRRSAVMSVSCYVQDLITITFLTYTANTYIPIHLPPL 75  
Db 22 QKVPTSKPPFTVGDIKKAIPHCQFQSLRFSYVYVDLILVSIMYYVANTYFHLPLSPY 81  
QY 76 VYLAMPVYWFQSCILITGLWLVGHCHGHAHSEYQWIDNAVGVFLHLSALLTPYFQWKYSH 135  
Db 82 CYIAWPIYWIQCGCVCTGIWVNAHCHGHAHSEYQWIDNAVGVFLHLSALLTPYFQWKYSH 141  
QY 136 RKHHANTNSLENEEYVYIPRTQSOLATYTYEFLDNTPGRIILVIMLTGLFPPLYLTTNVS 195  
Db 142 RRHHSNTGSLERDEVFPKPKSOLGWSKY--LNNPPGRVLSLTITLTGLWPLYLAFNVS 199  
QY 196 GKYYDRFTNHPDPLSPIETERERIQVALSDLGIVAFVGLKPLVOTKPGWVMQWYGPV 255  
Db 200 GRPYDRFACHYDPYGPYNNRERLQIFISDAGVLGVCYLLYRIALVKGLAMLCVYGVPL 259  
QY 256 IGLNSFIIVITVYLHHTLSSPHYSTENWIKGALTITDRDFGLNLRVFDVTHVTHV 315  
Db 260 LVNGLFLVLTLYLQHTQPSLPHYDSTEWDLRGALATCDRDYGVNLKVFHNITDTHVVHH 319  
QY 316 LFPYIPHYHAKESBAIKPILGDYRMIORTPFFKAMWEAKECIYEQDADSKHGTWY 375  
Db 320 LFTMPHYNAMEATKAIPKLLGDYYPDGTPTIYKEMWEAKECIYKEDSSQGGKGVWY 379

RESULT 7  
US-09-161-994A-16  
; Sequence 16, Application US/09161994A  
; Patent No. 6333448  
; GENERAL INFORMATION:  
; APPLICANT: BAFOR, Maureen  
; APPLICANT: BANAS, Antoni  
; APPLICANT: DAHLQVIST, Anders  
; APPLICANT: GUMMELSON, Per-Olov  
; APPLICANT: LEE, Michael  
; APPLICANT: SJODAL, Staffan  
; APPLICANT: STYMNE, Sten  
; APPLICANT: LENMAN, Marit  
; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF  
; FILE REFERENCE: BAFOR=1  
; CURRENT APPLICATION NUMBER: US/09/161,994A  
; CURRENT FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 9601236.4  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-161-994A-16  
Query Match 60.9%; Score 1271; DB 2; Length 383;  
Best Local Similarity 58.3%; Pred. No. 1.1e-122;  
Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;  
QY 16 ERAPIDPAPPSLSDLKKAIPAHCFRRSAVMSVSCYVQDLITITFLTYTANTYIPIHLPPL 75  
Db 22 QKVPTSKPPFTVGDIKKAIPHCQFQSLRFSYVYVDLILVSIMYYVANTYFHLPLSPY 81  
QY 76 VYLAMPVYWFQSCILITGLWLVGHCHGHAHSEYQWIDNAVGVFLHLSALLTPYFQWKYSH 135



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Db 82 CYTANPIYICQCVCTGIWVNAHECGHAFSDYQWVDDTVGLILHSALLVPVFSWKYSH 141
Qy 136 RKHANTNSLENEBEVYIPRTQSQRTYSTYEFDLNTPGRILILVIMLTGLGFPLYLITNVS 195
Db 142 RRHNSHTSGSLERDEVFPKPSQLGWSKY--LNNPPGRVLSLTITLTGLWPLYLAFNVS 199
Qy 196 GKXDRFTWHFDPLSFIFTERERIQVALSDLGIVAVPYGLKFLVQTKGFGWVCMYGVVP 255
Db 200 GRPYDRFACHYDPGYPIYNNRRLQIFISDAGVLGVCYLLYRIALVKGLAWLVCYGVPL 259
Qy 256 IGLNSFIIVITYLHHTHLSPPHYDSTENWIKGALTIDRDFGLLNRFVHDVTHVLHH 315
Db 260 LVVNGFLVITYLQHTHPSLPHYDSTENWLRGALATCDRDYGLNKFVHNITDTHVHH 319
Qy 316 LPFYIPHYHAKASEAIKPIGLDYRMDRTPFFKAMWREAKECIYIEQADSKHGTYWY 375
Db 320 LFTSMPHYNAPEATKAVKPLGIDYQFDGTPYIKENWREAKECLYVEKDESSQKGKGFVWY 379

RESULT 8
US-09-059-769-11
; Sequence 11, Application US/09059769
; Patent No. 6329518
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lenman, Marit
; APPLICANT: Styvne, Sten
; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,769
; FILING DATE: April 14, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P06223
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P06226
; FILING DATE: 15-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/043706
; FILING DATE: 16-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/050403
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
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; ORGANISM: Glycine max
US-09-059-769-11
Query Match 59.2%; Score 1234; DB 2; Length 383;
Best Local Similarity 57.0%; Pred. No. 7.2e-119;
Matches 211; Conservative 68; Mismatches 89; Indels 2; Gaps 1;

Qy 7 DRMKOHMDERAPIDPAPFSLDLKKAIPAHCRRSAVWSSCYVVOODLIITFLLYTVANT 66
Db 13 NRKSEVDPLKRVFPFEPKQFSLQIKKAIPPHCFQSRVLSRFSYVVDLTIAFLCYVATH 72
Qy 67 YIPLHPPPLVYLAWPVYFQCSCILTGLWVLGHECGHAFSEYQWIDNNAVGVFLHSALLT 126
Db 73 YFHLPPGPFUSFGMAIYAVQGCILTGVWVIAHECGHAFSDYQLDLDIIVGLILHSALLV 132
Qy 127 PYFSWKYSHRKHANTNSLENEBEVYIPRTQSQRTYSTYEFDLNTPGRILILVIMLTGLF 186
Db 133 PYFSWKYSHRHHNSHTSGSLERDEVFPKPSQLGWSKY--LNNPPGRVLTAVTLTGLW 190
Qy 187 PLYLLTNVSGKDYDRFTNHFDPISPIPTERRERIQVALSDLGIVAVPYGLKFLVQTKGFGW 246
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Qy 247 VMCYGVPIVGLNSFIIVITYLHHTHLSPPHYDSTENWIKGALTIDRDFGLLNRFVHD 306
Db 251 VVCVGVPLLVVNGFLVITYLQHTHPSLPHYDSTENWLRGALATCDRDYGLNKFVHN 310
Qy 307 VTHTHVLHLPYIPHYHAKASEAIKPIGLDYRMDRTPFFKAMWREAKECIYIEQAD 366
Db 311 IDTTHVAHLFSTMPHYHAMEATKAIKPIGLGEYRDETFPVKAMWREAKECIYIEVDPQS 370
Qy 367 SKHKGTYWYH 376
Db 371 TESKGVFWYN 380

RESULT 9
US-09-161-994A-15
; Sequence 15, Application US/09161994A
; Patent No. 6333448
; GENERAL INFORMATION:
; APPLICANT: BAFOR, Maureen
; APPLICANT: BANAS, Antoni
; APPLICANT: DAHLQVIST, Anders
; APPLICANT: GUMMESON, Per-Olov
; APPLICANT: LEE, Michael
; APPLICANT: SJODAL, Staffan
; APPLICANT: STYVNE, Sten
; APPLICANT: LENMAN, Marit
; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: BAFOR=1
; CURRENT APPLICATION NUMBER: US/09/161,994A
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 9601236.4
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Glycine max
US-09-161-994A-15
Query Match 59.2%; Score 1234; DB 2; Length 383;
Best Local Similarity 57.0%; Pred. No. 7.2e-119;
Matches 211; Conservative 68; Mismatches 89; Indels 2; Gaps 1;

Qy 7 DRMKOHMDERAPIDPAPFSLDLKKAIPAHCRRSAVWSSCYVVOODLIITFLLYTVANT 66
Db 13 NRKSEVDPLKRVFPFEPKQFSLQIKKAIPPHCFQSRVLSRFSYVVDLTIAFLCYVATH 72
Qy 67 YIPLHPPPLVYLAWPVYFQCSCILTGLWVLGHECGHAFSEYQWIDNNAVGVFLHSALLT 126
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Db 73 YFHLPGPLSPRGMAIYWAQVCILITGVWVIAHECGHAFSDYQLDDIVGLILHSALLV 132  
Qy 127 PYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPF 186  
Db 133 PYFSWKYSHRHRHSNTGLERDEVPKQKCIWKYSKY--LNNPPGRVLTAVTLTGLW 190  
Qy 187 PLYLLTNVSGKKYDRFTNHFPLSPITFERERIOVALSDLGIVAVFYGLKFLVQTKGFGW 246  
Db 191 PLYLALNVSGRPYDFACHYDYGPIYSDRERLQIYISDAGVLAIVVYGLFRILAMAKGLAW 250  
Qy 247 VMCYGVPIGLNSFIIVITVYLLHHTLSSPHYDSTENWIKGALTITDRDFGLLNRFVHD 306  
Db 251 VVCYGVPLLVNGFLVLTITFLOHTHPALPHYTSSEWDLRGALATVDRDYGILNKVFN 310  
Qy 307 VTHTVLHLLPPIPHYHAKESAIAKPILDYRMIDRTPPFKAMWREAKECIYEQDAD 366  
Db 311 ITDTHVAHLLFSTMPHYHAMEATKAIPILGEYRFDETPFVKAMWREARECIYVEPDQS 370  
Qy 367 SKHKGTYWYH 376  
Db 371 TESKGVFWYN 380  
RESULT 10  
US-09-837-751-31  
; Sequence 31, Application US/09837751  
; Patent No. 6974898  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-837-751-31  
Query Match 59.2%; Score 1234; DB 2; Length 383;  
Best Local Similarity 57.0%; Pred. No. 7.2e-119;  
Matches 211; Conservative 68; Mismatches 89; Indels 2; Gaps 1;

Qy 7 DRMKDHDDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDILITELLYTVANT 66  
Db 13 NRKSEVDPLKRVFPFKPQPSLQIKAIPPHCFORSVLSRFSYVYDLTIAFLYVATH 72  
Qy 67 YIPLPPLPVLAWPVYFCQSCILITGLWLVGHECGHAFSEYQWIDNAVGVPLHSALIT 126  
Db 73 YFHLPGPLSPRGMAIYWAQVCILITGVWVIAHECGHAFSDYQLDDIVGLILHSALLV 132  
Qy 127 PYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGPF 186  
Db 133 PYFSWKYSHRHRHSNTGLERDEVPKQKCIWKYSKY--LNNPPGRVLTAVTLTGLW 190  
Qy 187 PLYLLTNVSGKKYDRFTNHFPLSPITFERERIOVALSDLGIVAVFYGLKFLVQTKGFGW 246  
Db 191 PLYLALNVSGRPYDFACHYDYGPIYSDRERLQIYISDAGVLAIVVYGLFRILAMAKGLAW 250  
Qy 247 VMCYGVPIGLNSFIIVITVYLLHHTLSSPHYDSTENWIKGALTITDRDFGLLNRFVHD 306  
Db 251 VVCYGVPLLVNGFLVLTITFLOHTHPALPHYTSSEWDLRGALATVDRDYGILNKVFN 310  
Qy 307 VTHTVLHLLPPIPHYHAKESAIAKPILDYRMIDRTPPFKAMWREAKECIYEQDAD 366  
Db 311 ITDTHVAHLLFSTMPHYHAMEATKAIPILGEYRFDETPFVKAMWREARECIYVEPDQS 370

Qy 367 SKHKGTYWYH 376  
Db 371 TESKGVFWYN 380  
RESULT 11  
US-09-837-751-6  
; Sequence 6, Application US/09837751  
; Patent No. 6974898  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Gossypium sp.  
US-09-837-751-6  
Query Match 58.8%; Score 1226; DB 2; Length 383;  
Best Local Similarity 56.9%; Pred. No. 4.8e-118;  
Matches 205; Conservative 72; Mismatches 81; Indels 2; Gaps 1;  
Qy 16 ERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDILITELLYTVANTYIPLPPL 75  
Db 22 KRVYSKPPFTLSEIKKAIPPHCFORSVLSRFSYVYDLTIAFLYVATHYFVFNLPQAL 81  
Qy 76 VYLAWPVYFCQSCILITGLWLVGHECGHAFSEYQWIDNAVGVPLHSALLTPYFSWKYSH 135  
Db 82 SNVAPLYWAMQGCILITGVWVIAHECGHAFSDYQWLDLTVGLILHSSLLVPYFSWKYSH 141  
Qy 136 RKHANTNSLENEEVIPRTQSQLRTYSTYEFIDNTPGRIILIVIMLTGFLPILTNVS 195  
Db 142 RRHSNTGLERDEVPKQKCIWKYSKY--FNNPPGRFLSITITLGLMPLYLAFNVA 199  
Qy 196 GKVDRTNHFPLSPITFERERIOVALSDLGIVAVFYGLKFLVQTKGFWCMYGVVPV 255  
Db 200 GRPYDFACHYDYGPIYSDRERLQIYISDAGVLAIVVYGLFRILAMAKGVWISYGVPL 259  
Qy 256 IGLNSFIIVITVYLLHHTLSSPHYDSTENWIKGALTITDRDFGLLNRFVHDVTHVTLHH 315  
Db 260 LVNNAFLVMTIYLTQHTHPSLPHYDSSEWDMRGALSTVDRDYGILNKVFNITDTHVAH 319  
Qy 316 LPYIPHYHAKESAIAKPILDYRMIDRTPPFKAMWREAKECIYEQDADSKHKGTYWY 375  
Db 320 LFTMPHYHAMVATKAIPILGEYRFDGMPVYKAIWREAKECELYVEPDGDKGVPMF 379  
RESULT 12  
US-08-872-302-2  
; Sequence 2, Application US/08872302  
; Patent No. 5846784  
; GENERAL INFORMATION:  
; APPLICANT: Hitz, William D  
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
; TITLE OF INVENTION: Developing Seeds of Vernonia galamensis  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. duPont de Nemours and Co.  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19898  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,302
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R
; REGISTRATION NUMBER: P-41,173
; REFERENCE/DOCKET NUMBER: BB-1084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-872-302-2

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|                       |        |              |           |            |        |        |    |      |    |
|-----------------------|--------|--------------|-----------|------------|--------|--------|----|------|----|
| Query Match           | 58.7%; | Score        | 1224.5;   | DB 1;      | Length | 382;   |    |      |    |
| Best Local Similarity | 56.6%; | Pred. No.    | 6.9e-118; |            |        |        |    |      |    |
| Matches               | 206;   | Conservative | 72;       | Mismatches | 83;    | Indels | 3; | Gaps | 2; |

  

|    |     |                     |   |         |    |
|----|-----|---------------------|---|---------|----|
| Qy | 16  | ERAPIDPAPFSLDKKAI   | PAHCFRRSAVSSCVVODLIITFLTYVTANTYI                | PHLPPL  | 75 |
| Db | 21  | ERYPAKPPPTISDLKKAIP | HCQFRLRSFSVVDVLAVSFLLTYVAATY                    | FHHLPNF | 80 |
| Qy | 76  | VYLAWPYWFCQSCIL     | TGLWLGHECHGHAFSEYQWIDNAGVFLHSGALLTPYFSWKYSH     | 135     |    |
| Db | 81  | SSLAWLAYVWVGCVL     | TGVMVIAHECHGHAFSDYQWVDDTVGFLHSLVLLVPFWSWKYSH    | 140     |    |
| Qy | 136 | RKHANTNSLENBEVYI    | PRTQSQLRTYSTVEFLDNTQGRILILVIMLTIGPPLVLLTNVS     | 195     |    |
| Db | 141 | RRHSNTSGLERDEVF     | YFKPSRKIPWYSKY--FNNAPGRMMSVFETTLTGLMPLYLNVNS    | 198     |    |
| Qy | 196 | GKKYDRFTNHFDP       | LSPIFTFERERIQVALSDLGIVAVFYGLKFLVQTGKGFVGMCMYGVV | 255     |    |
| Db | 199 | GRPYDRFACHFS        | PNSPYNERERLIWLSDLGMTSMSPILYRVAVAGVAWVICMYGIPL   | 258     |    |
| Qy | 256 | IGLNSPIVITYLHHT     | LSSPHYDSTEWNIKGAATTIDRDFGLLNRVFHDVTHVLLHH       | 315     |    |
| Db | 259 | LI VNGFLVTITYLQ     | HTHPSLFHYDSSSEWDLRGAMATVDRDYGVLNVKVFHNITDTHVVHH | 318     |    |
| Qy | 316 | LPFYIPHYHAKASEA     | LKPILDGYRMTDRTPFFKAMWREAKECIVYIBQADSKHKGTWY     | 375     |    |
| Db | 319 | LFSTMPHYNAMEAT      | KAVKPLGLEYQFDGTPFYVAIWREAKECULFVDPDEGEGOGGVFWY  | 378     |    |
| Qy | 376 | -HKM                | 378   |         |    |
| Db | 379 | KNKM                | 382   |         |    |

RESULT 13  
US-08-314-596-41  
; Sequence 41, Application US/08314596  
; Patent No. 5668292  
; GENERAL INFORMATION:  
; APPLICANT: SOMERVILLE, CHRIS  
; APPLICANT: VAN DE LOO, FRANK  
; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/314,596  
FILING DATE: 26-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 206905/1220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 383 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-314-596-41

| Query Match           | 58.2%;           | Score 1215;   | DB 1;     | Length 383; |
|-----------------------|------------------|---|-----------|-------------|
| Beat Local Similarity | 55.6%;           | Pred. No. 6.6e-117;   |           |             |
| Matches 205;          | Conservative 70; | Mismatches 92;  | Indels 2; | Gaps 1;     |
| QY                    | 8                | RMKDHDMDERAPIDAPFSLSDLKKAIPAHCFRRSAVWSSCYVQDILITFLLYTVANTY    | 67        |             |
| DB                    | 14               | KKSTDTTKRVCKBPSPFVGDLLKALPPHCFKRSIPRSPFSLISDIIIASCFYVATNY     | 73        |             |
| QY                    | 68               | IPHLPPPLVYLAWPVYFPCOSCILTGLWLGHCEGHHAFSEYOWIDNAVGFVLHSALLTP   | 127       |             |
| DB                    | 74               | PSLLPQPLSYLAWPLYWACQCVLTGIWVAHECGHAFSDYQWLDTDVGLIFHSFLLP      | 133       |             |
| QY                    | 128              | YFSWKYSHRKHKHAANTSLENEEYVIPRTQSOLRYSITYEFLDNTPTGRILLIVMLTGLGP | 187       |             |
| DB                    | 134              | YFSWKYSHRRHSNTGSLERDEVFVPKQSAIKYGYK--LNNPLGRIMMLTVQFVLGWP     | 191       |             |
| QY                    | 188              | LYLLTNSVGKKYDRFTNHPFLOPSIFETERRIQVALSDLGIVAFYGLKFLVQTKGFQW    | 247       |             |
| DB                    | 192              | LYLAFNVSGRPYDGFACHFFPNAPIYNDRLRLQIYLSDAGILAVCFGLYRYAAQGWASM   | 251       |             |
| QY                    | 248              | MCMTGVPIVGNLSFIIVITLYLHHTLSSPHYDSTEWNIKGLATTIIRDPGLINRVPHDV   | 307       |             |
| DB                    | 252              | ICLYGVPLLIYNAPFLVITLYQHTPHSLPHYDSSWDWLRGALATVDRDYDGLINKVPHNI  | 311       |             |
| QY                    | 308              | THTHVLHHLPPYIIPHYHAKASEAIKPILDGYRMIIDRTPPFKMWREAKECIYIEQDADS  | 367       |             |
| DB                    | 312              | TDTHVAHHLFSTMPHYNAMEATKAIKPILDGYQFDGTPYVAVMYREAKECIYIEVPBREG  | 371       |             |
| QY                    | 368              | KHKGTYYWH   | 376       |             |
| DB                    | 372              | DKKGYYWYN   | 380       |             |

RESULT 14  
US-08-320-982-41  
; Sequence 41, Application US/08320982  
; Patent No. 5801026  
; GENERAL INFORMATION:  
; APPLICANT: SOMERVILLE, CHRIS  
; APPLICANT: VAN DE LOO, FRANK  
; TITLE OF INVENTION: USE OF PLANT  
; TITLE OF INVENTION: PRODUCE HYDR  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUS  
; STREET: 1100 NEW YORK AVENUE,  
; CITY: WASHINGTON  
; STATE: D.C.

APPLICANT: VAN DE LEE, FRANK.  
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:34:21 ; Search time 198 Seconds  
(without alignments)  
872.868 Million cell updates/sec

Title: US-10-622-774-2

Perfect score: 2086

Sequence: 1 MSDSVYDRMKDHMDERAPI.....IYEQDADSKHGTWYHQM 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_8.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*  
10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description        |
|------------|--------|-------------|--------|-------|--------------------|
| 1          | 2086   | 100.0       | 378    | 9     | Adw68587 Stokesia  |
| 2          | 2077   | 99.6        | 378    | 9     | Aec02369 Stokesia  |
| 3          | 1821   | 87.3        | 384    | 2     | Aaw83354 Vernonia  |
| 4          | 1549.5 | 74.3        | 377    | 8     | Adr87355 Hydroxyla |
| 5          | 1549.5 | 74.3        | 377    | 8     | Adr87357 Codon opt |
| 6          | 1549.5 | 74.3        | 377    | 8     | Adr87361 Codon opt |
| 7          | 1549.5 | 74.3        | 377    | 9     | Aec02271 Stokesia  |
| 8          | 1549.5 | 74.3        | 377    | 9     | Aec02275 Stokesia  |
| 9          | 1549.5 | 74.3        | 377    | 9     | Aec02269 Stokesia  |
| 10         | 1523.5 | 73.0        | 377    | 4     | Aab70946 C. offici |
| 11         | 1510   | 72.4        | 374    | 2     | Aaw79743 Crepis sp |
| 12         | 1504   | 72.1        | 374    | 8     | Adr87360 Codon opt |
| 13         | 1504   | 72.1        | 374    | 9     | Aec02274 Crepis bi |
| 14         | 1499   | 71.9        | 374    | 9     | Aec02370 Crepis bi |
| 15         | 1498   | 71.8        | 374    | 8     | Adr87337 Hydroxyla |
| 16         | 1498   | 71.8        | 374    | 9     | Aec02251           |
| 17         | 1497   | 71.8        | 374    | 9     | Aec02368           |
| 18         | 1493   | 71.6        | 374    | 2     | Aaw79742 Crepis pa |
| 19         | 1493   | 71.6        | 374    | 8     | Adr87450 Crepis pa |
| 20         | 1482   | 71.0        | 380    | 8     | Adr87343 FAD2/Hydr |
| 21         | 1482   | 71.0        | 380    | 9     | Aec02257 Crepis bi |
| 22         | 1458   | 69.9        | 372    | 9     | Adx69239 Delta-12  |
| 23         | 1458   | 69.9        | 372    | 9     | Adx85618 C. palae  |

|    |        |      |     |   |          |           |
|----|--------|------|-----|---|----------|-----------|
| 24 | 1458   | 69.9 | 372 | 9 | Adw88814 | C. palae  |
| 25 | 1427.5 | 68.4 | 375 | 2 | Aaw36793 | Crepis al |
| 26 | 1424.5 | 68.3 | 375 | 9 | Adx18010 | Crepis al |
| 27 | 1424.5 | 68.3 | 375 | 9 | Adx69237 | Delta-12  |
| 28 | 1424.5 | 68.3 | 375 | 9 | Adx85616 | C. alpina |
| 29 | 1279   | 61.3 | 383 | 4 | Aay72825 | Borago of |
| 30 | 1263   | 60.5 | 392 | 8 | Adx93353 | Plant ful |
| 31 | 1263   | 60.5 | 395 | 8 | Adx71277 | Plant ful |
| 32 | 1258   | 60.3 | 383 | 8 | Ado14197 | Sesamum i |
| 33 | 1258   | 60.3 | 383 | 8 | Adr87447 | Hydroxyla |
| 34 | 1258   | 60.3 | 383 | 9 | Aec02361 | Sesamum i |
| 35 | 1248   | 59.8 | 387 | 7 | Ad840489 | P. granat |
| 36 | 1242.5 | 59.6 | 383 | 5 | Aag80695 | C. offici |
| 37 | 1242.5 | 59.6 | 383 | 9 | Aec96301 | Calendula |
| 38 | 1234   | 59.2 | 383 | 4 | Aae13427 | Soybean m |
| 39 | 1234   | 59.2 | 383 | 8 | Adr87446 | Hydroxyla |
| 40 | 1234   | 59.2 | 383 | 9 | Aec02360 | Glycine m |
| 41 | 1226   | 58.8 | 383 | 4 | Aae13421 | Cotton ol |
| 42 | 1224.5 | 58.7 | 382 | 2 | Aaw83353 | Vernonia  |
| 43 | 1222   | 58.6 | 383 | 2 | Aay50098 | Arabidops |
| 44 | 1221.5 | 58.6 | 386 | 8 | Adt58651 | Plant pol |
| 45 | 1215   | 58.2 | 377 | 3 | Aag22054 | Arabidops |

#### ALIGNMENTS

RESULT 1

Adw68587  
ID Adw68587 standard; protein; 378 AA.

AC Adw68587;

DT 07-APR-2005 (first entry)

DE Stokesia laevis fatty acid epoxigenase protein.

KW DNA purification; transgenic plant; plant; expression; recombinant DNA;

KW seed oil; soybean oil; linseed oil; plastic;

KW delta 12-fatty acid epoxigenase; delta 12-epoxigenase;

KW delta 12-epoxidase; enzyme; transgenic.

OS Stokesia laevis.

XX US2005022270-A1.

PN 27-JAN-2005.

PD 21-JUL-2003; 2003US-00622774.

XX 21-JUL-2003; 2003US-00622774.

XX (HILD/) HILDEBRAND D.

PA (HATA/) HATANAKA T.

XX Hildebrand D, Hatanaka T;

PI WPI: 2005-111979/12.

XX N-PSDB; Adw68586.

DR New isolated nucleic acid molecule encoding a delta 12-fatty acid

XX epoxigenase enzyme, useful for genetically producing industrial products

PT including coating, composites, adhesives and plasticizers.

XX Claim 1; SEQ ID NO 2; 22pp; English.

PS The present invention relates to a nucleic acid molecule encoding a delta

XX 12-fatty acid epoxigenase enzyme. The invention is useful for genetically

CC producing raw materials in the manufacture of industrial products

CC including coating, composites, adhesives and plasticizers. The present

CC sequence is the Stokesia laevis fatty acid epoxigenase protein.

XX Sequence 378 AA;

SQ

Query Match 100.0%; Score 2086; DB 9; Length 378;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-215;  
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60  
 Db 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60

Qy 61 YTVANTYIPLPPLVYLAWPVYWCQSCILTLGLWVLGHECHGHAFAFSEYQWIDNAGFVL 120  
 Db 61 YTVANTYIPLPPLVYLAWPVYWCQSCILTLGLWVLGHECHGHAFAFSEYQWIDNAGFVL 120

Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYVEFLDNTPGRIILIVI 180  
 Db 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYVEFLDNTPGRIILIVI 180

Qy 181 MTLGFPPLYLTLNVSGKKYDRFTNHFDPISLPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240  
 Db 181 MTLGFPPLYLTLNVSGKKYDRFTNHFDPISLPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240

Qy 241 TKFGVWCMYGVPIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300  
 Db 241 TKFGVWCMYGVPIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300

Qy 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPILDGYRIMIDRTPPFKAMWREAKECIY 360  
 Db 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPILDGYRIMIDRTPPFKAMWREAKECIY 360

Qy 361 IEQDADSKHKGTYYWHKM 378  
 Db 361 IEQDADSKHKGTYYWHKM 378

RESULT 2  
 AEC02369  
 ID AEC02369 standard; protein; 378 AA.  
 AC AEC02369;  
 DT 06-OCT-2005 (first entry)  
 DE *Stokesia laevis* epoxigenase SEQ ID NO.136.  
 KW transgenic plant; anhelmintic; epoxigenase.  
 OS *Stokesia laevis*.  
 XX US2005172358-A1.  
 XX 04-AUG-2005.  
 XX 04-AUG-2004; 2004US-00912534.  
 XX 04-FEB-2004; 2004US-00772227.  
 XX (VERB/) VERBSKY M L.  
 XX (BAUB/) BAUBLITE C.  
 XX (KLOE/) KLOEK A P.  
 XX (DAVI/) DAVILA-APONTE J A.  
 XX (HRES/) HRESKO M C.  
 XX (MCLA/) MCLAIRD M B.  
 XX (ZENT/) ZENTELLA R.  
 XX (WILL/) WILLIAMS D J.  
 XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;  
 XX Mcleird MB, Zentella R, Williams DJ;  
 XX WPI; 2005-603337/62.  
 XX N-PSDB; AEC02364.  
 XX New transgenic plant having a DNA construct comprising a nucleic acid  
 XX encoding a protein for catalyzing the conversion of a substrate to a C16,

PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
 PT anhelmintic compounds.  
 XX Claim 21; SEQ ID NO 136; 130pp; English.  
 XX The invention relates to a transgenic plant containing at least one DNA  
 CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
 CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
 CC monounsaturated fatty acid product; and (b) a regulatory element operably  
 CC linked to the nucleic acid encoding the polypeptide and conferring  
 CC expression in a vegetative tissue of the plant. Also described: (1) a  
 CC method of making a transgenic plant; (2) an isolated nucleic acid  
 CC comprising the nucleotide sequence; (3) a recombinant nucleic acid  
 CC construct comprising at least one regulatory element that confers  
 CC expression in a vegetative tissue of a plant; and (4) a method of  
 CC screening a transgenic plant for anhelmintic activity. The transgenic  
 CC plant is useful in preparing compounds having anhelmintic activity. The  
 CC present sequence represents an epoxigenase which is used in the  
 CC exemplification of the present invention.  
 XX Sequence 378 AA;  
 SQ

Query Match 99.6%; Score 2077; DB 9; Length 378;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-214;  
 Matches 376; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60  
 Db 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRAVWSSCYVQDLIIITFL 60

Qy 61 YTVANTYIPLPPLVYLAWPVYWCQSCILTLGLWVLGHECHGHAFAFSEYQWIDNAGFVL 120  
 Db 61 YTVANTYIPLPPLVYLAWPVYWCQSCILTLGLWVLGHECHGHAFAFSEYQWIDNAGFVL 120

Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYVEFLDNTPGRIILIVI 180  
 Db 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPRTQSQLRTYSTYVEFLDNTPGRIILIVI 180

Qy 181 MTLGFPPLYLTLNVSGKKYDRFTNHFDPISLPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240  
 Db 181 MTLGFPPLYLTLNVSGKKYDRFTNHFDPISLPIFTRERERIOVALSDLGIVAVFYGLKFLVQ 240

Qy 241 TKFGVWCMYGVPIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300  
 Db 241 TKFGVWCMYGVPIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTIDRDFGL 300

Qy 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPILDGYRIMIDRTPPFKAMWREAKECIY 360  
 Db 301 NRVFHDVTHVHLHLPFYIPIHYHAKASEAIKPILDGYRIMIDRTPPFKAMWREAKECIY 360

Qy 361 IEQDADSKHKGTYYWHKM 378  
 Db 361 IEQDADSKHKGTYYWHKM 378

RESULT 3  
 AAW83354  
 ID AAW83354 standard; protein; 384 AA.  
 XX AAW83354;  
 XX 27-AUG-2003 (revised)  
 XX 10-FEB-1999 (first entry)  
 XX Vernonia galamenensis fatty acid epoxidising enzyme.  
 XX Vernonia galamenensis; fatty acid desaturase; epoxidising enzyme;  
 XX expression; chimeric gene; recombinant enzyme.  
 XX Vernonia galamenensis.  
 XX US5846784-A.  
 XX



Db 180 RLTLGPPPLVLTNTSGKKYQFANHPDPLSPDIFTERERIQVLVSDGLLAVIYAKLLVA 239

Qy 241 TKRGWVMCMYGVPIGLNSPIIIVITLHHTLSSPHYDSTENWIKGALTIDRDFGLL 300

Db 240 AKGAVWVTCIYGVPIGLNSPIIIVITLHHTLSSPHYDSTENWIKGALTIDRDFGLL 299

Qy 301 NRVFHDVTHVTHLHLLFPYIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 360

Db 300 NRVFHDVTHVTHLHLLFPYIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 359

Qy 361 IEQDADSKHGKGYWYHKM 378

Db 360 IEPDEDEHKGYWYHKM 377

RESULT 5

ADR87357

ID ADR87357 standard; protein; 377 AA.

XX

AC ADR87357;

DT 18-NOV-2004 (first entry)

XX

DE Codon optimised hydroxylase/ epoxigenase, SEQ ID 38.

XX

KW Nematocite; Plant; 16C monounsaturated fatty acid;

KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;

KW fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;

KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;

KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;

XX

OS Stokesia laevis.

OS Synthetic.

XX

PN WO2004071168-A2.

PD 26-AUG-2004.

PF 04-FEB-2004; 2004WO-US003254.

PR 05-FEB-2003; 2003US-0445293P.

XX

PA (DIVE-) DIVERGENCE INC.

XX

PI Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;

PI Hresko MC, McLaird MB, Zentella R;

XX

DR WPI; 2004-634973/61.

DR N-P8DB; ADR87348.

XX

PT Novel transgenic plant containing DNA construct having nucleic acid

PT encoding polypeptide for catalyzing conversion of substrate to

PT monounsaturated fatty acid product, useful for controlling nematodes.

XX

PS Claim 21; SEQ ID NO 38; 180pp; English.

CC

CC The present invention relates to transgenic plants (I) containing one or

CC more DNA constructs. The DNA constructs have a nucleic acid encoding a

CC protein effective for catalyzing the conversion of a substrate to a 16C,

CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid

CC epoxigenase or a fatty hydroxylase, and a regulatory element operably

CC linked to the nucleic acid encoding the protein, where the regulatory

CC element confers expression in vegetative tissue of the plant. The fatty

CC acid epoxigenase or a fatty hydroxylase can be

CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol

CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty

CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in

CC a vegetative tissue. The DNA construct of (I) is useful in the production

CC of hydroxylases and epoxigenases that controls nematode damage in

CC commercially important plant species and so (I) exhibits increased

CC resistance to nematodes. (I) provides an effective, environmentally safe

CC methods of inhibiting nematode metabolism, growth, viability,

CC development, infectivity and/or the nematode life cycle. (I) provides

CC season-long nematode control, thus providing labor savings, by reducing

CC the need for and frequency of chemical control. The present sequence is

CC one such fatty acid epoxigenase and fatty hydroxylase, which has been

CC codon optimised for improved plant expression.

XX

SEQ Sequence 377 AA;

Query Match 74.3%; Score 1549.5; DB 8; Length 377;

Best Local Similarity 72.0%; Pred. No. 9.8e-158;

Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRERSAYWSSCYVVDLIITFL 60

Db 7 MSDLSGK-----NLTAKRVPDP-PFTLSIDIKALPPHCFRKSVIRSSYYVVDLIVSYF 61

Qy 61 YTVANTYIPLPPLVYLAMPVYWFQSCILITGLWVLCGHCCHAFSEYQWIDNAVGPVL 120

Db 62 PFLATTYITVLPAPLAYIAMPVYWFQSCILITGLWVLCGHCCHAFSEYQWIDDTVGFL 121

Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSLRTYTYSEFLDNTPGRLILVI 180

Db 122 HSALLTPYFSWKYSHRKHANTNSLDNDEVYIPKRKSKVIYS--KILNPPGRVFTLVF 179

Qy 181 MLTGLPPLVLTNTSGKKYQFANHPDPLSPDIFTERERIOVALSDLGIVAVFYGLKPLVQ 240

Db 180 RLTLGPPPLVLTNTSGKKYQFANHPDPLSPDIFTERERIOVLVSDGLLAVIYAKLLVA 239

Qy 241 TKRGWVMCMYGVPIGLNSPIIIVITLHHTLSSPHYDSTENWIKGALTIDRDFGLL 300

Db 240 AKGAVWVTCIYGVPIGLNSPIIIVITLHHTLSSPHYDSTENWIKGALTIDRDFGLL 299

Qy 301 NRVFHDVTHVTHLHLLFPYIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 360

Db 300 NRVFHDVTHVTHLHLLFPYIHYHAKSEAIKPIGLGYRMDRTPPFKAMWREAKECIY 359

Qy 361 IEQDADSKHGKGYWYHKM 378

Db 360 IEPDEDEHKGYWYHKM 377

RESULT 6

ADR87361

ID ADR87361 standard; protein; 377 AA.

XX

AC ADR87361;

DT 18-NOV-2004 (first entry)

XX

DE Codon optimised hydroxylase/ epoxigenase, SEQ ID 42.

XX

KW Nematocite; Plant; 16C monounsaturated fatty acid;

KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;

KW fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;

KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;

KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;

KW nematode.

XX

OS Stokesia laevis.

OS Synthetic.

XX

PN WO2004071168-A2.

PD 26-AUG-2004.

PF 04-FEB-2004; 2004WO-US003254.

PR 05-FEB-2003; 2003US-0445293P.

XX

PA (DIVE-) DIVERGENCE INC.

XX

PI Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;

PI Hresko MC, McLaird MB, Zentella R;



```

XX WPI; 2004-634973/61.
DR N-PSDB; ADR87352.
XX
XX Novel transgenic plant containing DNA construct having nucleic acid
PT encoding polypeptide for catalyzing conversion of substrate to
PT monounsaturated fatty acid product, useful for controlling nematodes.
XX
XX Claim 21; SEQ ID NO 42; 180pp; English.
XX
XX The present invention relates to transgenic plants (I) containing one or
CC more DNA constructs. The DNA constructs have a nucleic acid encoding a
CC protein effective for catalyzing the conversion of a substrate to a 16C,
CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid
CC epoxigenase or a fatty hydroxylase, and a regulatory element operably
CC linked to the nucleic acid encoding the protein, where the regulatory
CC element confers expression in vegetative tissue of the plant. The fatty
CC acid epoxigenase or a fatty hydroxylase can be
CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol
CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty
CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in
CC a vegetative tissue. The DNA construct of (I) is useful in the production
CC of hydroxylases and epoxigenases that controls nematode damage in
CC commercially important plant species and so (I) exhibits increased
CC resistance to nematodes. (I) provides an effective, environmentally safe
CC methods of inhibiting nematode metabolism, growth, viability,
CC development, infectivity and/or the nematode life cycle. (I) provides
CC season-long nematode control, thus providing labor savings, by reducing
CC the need for and frequency of chemical control. The present sequence is
CC one such fatty acid epoxigenase and fatty hydroxylase, which has been
CC codon optimised for improved plant expression.
XX
XX Sequence 377 AA;
XX
Query Match 74.3%; Score 1549.5; DB 8; Length 377;
Best Local Similarity 72.0%; Pred. No. 9.8e-158;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;
QY 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCPRRSVAVWSSCVVQDLITFL 60
Db 7 MSDSLKGK----NLLKRVDP--PFTSLDKKAIPHCPRRSVIRSSVYVHDLIVSYVF 61
QY 61 YTVANTYIPLPPLVYLAWPVYVFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGFVL 120
Db 62 FFLATTIITVLPAPLAIAPVWVFCQASILTGLWLGHECGHAFSEYQWIDTGVFIL 121
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEYIPRTQSOLRTYSTYFELDNTPGRIILVI 180
Db 122 HSALLTPYFSWKYSHRKHANTNSLNDDEVYIPKRKSKVIYS--KILNPPGRVFTLVF 179
QY 181 MLTLGFPPLVLLTNVSGKCYDRFTNHPDPLSPIETERERIOVALSDLGIVAVFGKFLVQ 240
Db 180 RLTLGFPPLVLLTNVSGKCYDRFTNHPDPLSPIETERERIOVALSDLGIVAVFGKFLVQ 239
QY 241 TKGFGWCMYGVPIVGLNSFIITVILYHHTLSSPHYSTENWNWIKGALTTIDRDFGLL 300
Db 240 AKGAVWTCIYGVPLGVSVFFVLTITVHLHTLSLPHYDSTENWIRGALSTIDRDFGL 299
QY 301 NRVFHDVTHVTHLHLPPIYPHYHAKASEAIPILGDYRMDIRTPFFKAMWREAKECIY 360
Db 300 NRVFHDVTHVTHLHLSIYPHYHAKARDAIKPVLGDYKIDRTPIFKAMWREAKECIY 359
QY 361 IEODADSKHKGTYYVYHKM 378
Db 360 IEPEDETEHKGVYVYHKM 377
RESULT 7
ID AEC02271 standard; protein; 377 AA.
XX
XX AEC02271;
XX

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DT 06-OCT-2005 (first entry)
XX
XX Stokesia laevis epoxigenase SEQ ID NO:38.
XX
XX transgenic plant; anthelmintic; epoxigenase.
XX
XX Stokesia laevis.
XX
XX US2005172358-A1.
XX
XX 04-AUG-2005.
XX
XX 04-AUG-2004; 2004US-00912534.
XX
XX 04-FEB-2004; 2004US-00772227.
XX
XX (VERB/) VERBSKY M L.
XX (BAUB/) BAUBLITE C.
XX (KLOE/) KLOEK A P.
XX (DAVI/) DAVILA-APONTE J A.
XX (HRES/) HRESKO M C.
XX (MCLA/) MCLAIRD M B.
XX (ZENT/) ZENTELLA R.
XX (WILL/) WILLIAMS D J.
XX
XX Verbesky ML, Baublite C, Kloeck AP, Davila-Aponte JA, Hresko MC;
PI Mcclaird MB, Zentella R, Williams DJ;
XX
XX WPI; 2005-603337/62.
DR N-PSDB; AEC02262.
XX
XX New transgenic plant having a DNA construct comprising a nucleic acid
PT encoding a protein for catalyzing the conversion of a substrate to a C16,
PT C18 or C20 monounsaturated fatty acid product, useful in preparing
PT anthelmintic compounds.
XX
XX Claim 21; SEQ ID NO 38; 130pp; English.
XX
XX The invention relates to a transgenic plant containing at least one DNA
CC construct comprising: (a) a nucleic acid encoding a polypeptide effective
CC for catalyzing the conversion of a substrate to a C16, C18, or C20
CC monounsaturated fatty acid product; and (b) a regulatory element operably
CC linked to the nucleic acid encoding the polypeptide and conferring
CC expression in a vegetative tissue of the plant. Also described: (1) a
CC method of making a transgenic plant; (2) an isolated nucleic acid
CC comprising the nucleotide sequence; (3) a recombinant nucleic acid
CC construct comprising at least one regulatory element that confers
CC expression in a vegetative tissue of a plant; and (4) a method of
CC screening a transgenic plant for anthelmintic activity. The transgenic
CC plant is useful in preparing compounds having anthelmintic activity. The
CC present sequence represents an epoxigenase which is used in the
CC exemplification of the present invention.
XX
XX Sequence 377 AA;
XX
Query Match 74.3%; Score 1549.5; DB 9; Length 377;
Best Local Similarity 72.0%; Pred. No. 9.8e-158;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;
QY 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCPRRSVAVWSSCVVQDLITFL 60
Db 7 MSDSLKGK----NLLKRVDP--PFTSLDKKAIPHCPRRSVIRSSVYVHDLIVSYVF 61
QY 61 YTVANTYIPLPPLVYLAWPVYVFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGFVL 120
Db 62 FFLATTIITVLPAPLAIAPVWVFCQASILTGLWLGHECGHAFSEYQWIDTGVFIL 121
QY 121 HSALLTPYFSWKYSHRKHANTNSLENEEYIPRTQSOLRTYSTYFELDNTPGRIILVI 180
Db 122 HSALLTPYFSWKYSHRKHANTNSLNDDEVYIPKRKSKVIYS--KILNPPGRVFTLVF 179
QY 181 MLTLGFPPLVLLTNVSGKCYDRFTNHPDPLSPIETERERIOVALSDLGIVAVFGKFLVQ 240

```

Db 180 RLTGFPYLLTNTSGKKYQRFANHPDPLSPIFTRERIQVLVSDGLLAVIYAIKLVA 239  
 Qy 241 TKGFQWVMCMYGVPIVGLNSPIIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
 Db 240 AKGAVWVTCIYGVPLVGVSPFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299  
 Qy 301 NRVFHDVTHVHLHLPYIPHYHAKSEAIKPTILGDRMIDRTPPFKAMWREAKECIY 360  
 Db 300 NRVFHDVTHVHLHLSIYIPHYHAKSEARDAIKPVLGDYKIDRTPIPKAMWREAKECIY 359  
 Qy 361 IEQADSKHGKTYWYHKM 378  
 Db 360 IEPDETEHKGWYWYHKM 377  
 RESULT 8  
 AEC02275  
 ID AEC02275 standard; protein; 377 AA.  
 XX  
 AC AEC02275;  
 DT 06-OCT-2005 (first entry)  
 DE Stokesia laevis epoxigenase SEQ ID NO:42.  
 XX transgenic plant; anthelmintic; epoxigenase.  
 KW  
 OS Stokesia laevis.  
 XX  
 PN US2005172358-A1.  
 XX  
 PD 04-AUG-2005.  
 XX  
 PF 04-AUG-2004; 2004US-00912534.  
 PR 04-FEB-2004; 2004US-00772227.  
 PA (VERB/) VERBSKY M L.  
 PA (BAUB/) BAUBLITE C.  
 PA (KLOE/) KLOEK A P.  
 PA (DAVI/) DAVILA-APONTE J A.  
 PA (HRES/) HRESKO M C.  
 PA (MCLA/) MCLAIRD M B.  
 PA (ZENT/) ZENTELLA R.  
 PA (WILL/) WILLIAMS D J.  
 XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;  
 PI Mcclaird MB, Zentella R, Williams DJ;  
 XX  
 DR WPI; 2005-603337/62.  
 DR N-PSDB; AEC02266.  
 XX  
 PT New transgenic plant having a DNA construct comprising a nucleic acid  
 PT encoding a protein for catalyzing the conversion of a substrate to a C16,  
 PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
 PT anthelmintic compounds.  
 XX  
 PS Claim 21; SEQ ID NO 42; 130pp; English.  
 XX  
 CC The invention relates to a transgenic plant containing at least one DNA  
 CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
 CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
 CC monounsaturated fatty acid product; and (b) a regulatory element operably  
 CC linked to the nucleic acid encoding the polypeptide and conferring  
 CC expression in a vegetative tissue of the plant. Also described: (1) a  
 CC method of making a transgenic plant; (2) an isolated nucleic acid  
 CC comprising the nucleotide sequence; (3) a recombinant nucleic acid  
 CC construct comprising at least one regulatory element that confers  
 CC expression in a vegetative tissue of a plant; and (4) a method of  
 CC screening a transgenic plant for anthelmintic activity. The transgenic  
 CC plant is useful in preparing compounds having anthelmintic activity. The  
 CC present sequence represents an epoxigenase which is used in the  
 CC exemplification of the present invention.

XX Sequence 377 AA;  
 SQ  
 Query Match 74.3%; Score 1549.5; DB 9; Length 377;  
 Best Local Similarity 72.0%; Pred. No. 9.8e-158;  
 Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;  
 Qy 1 MSDSYDDRMKDMDERAPIDPAPFSLDLKKAIPAHCFRRAVSSCYVQDLIITPLL 60  
 Db 7 MSDSLSDGK- - - - -NLLKRPVDP- PFTLSIDIKKAIPHCFKRSVIRSSYYVHDLIVSYVF 61  
 Qy 61 YTVANTYIPHLPPPLVYLAWPVYWFQSCILTLGLWLGHEGCHHAFSEYQWIDNAVGFV 120  
 Db 62 PFLATTYITVLPAPLAYIANPVYWFQASILTGLWVGHEGCHHAFSEYQWIDTGVGFL 121  
 Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEVVIPTQSLRTYTYEFLDNTPPGRILILVI 180  
 Db 122 HSALLTPYFSWKYSHRNHANTNSLDNDEVVYIPKRKVKIYS- -KILNPPGRVFTLVF 179  
 Qy 181 MLTGLPPLYLLTNTSGKKYQRFANHPDPLSPIFTRERIQVALSDGLGVAVFYGLKELVQ 240  
 Db 180 RLTGFPYLLTNTSGKKYQRFANHPDPLSPIFTRERIQVLVSDGLLAVIYAIKLVA 239  
 Qy 241 TKGFQWVMCMYGVPIVGLNSPIIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
 Db 240 AKGAVWVTCIYGVPLVGVSPFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299  
 Qy 301 NRVFHDVTHVHLHLPYIPHYHAKSEAIKPTILGDRMIDRTPPFKAMWREAKECIY 360  
 Db 300 NRVFHDVTHVHLHLSIYIPHYHAKSEARDAIKPVLGDYKIDRTPIPKAMWREAKECIY 359  
 Qy 361 IEQADSKHGKTYWYHKM 378  
 Db 360 IEPDETEHKGWYWYHKM 377  
 RESULT 9  
 AEC02269  
 ID AEC02269 standard; protein; 377 AA.  
 XX  
 AC AEC02269;  
 DT 06-OCT-2005 (first entry)  
 DE Stokesia laevis epoxigenase SEQ ID NO:36.  
 XX transgenic plant; anthelmintic; epoxigenase.  
 KW  
 OS Stokesia laevis.  
 XX  
 PN US2005172358-A1.  
 XX  
 PD 04-AUG-2005.  
 XX  
 PF 04-AUG-2004; 2004US-00912534.  
 PR 04-FEB-2004; 2004US-00772227.  
 PA (VERB/) VERBSKY M L.  
 PA (BAUB/) BAUBLITE C.  
 PA (KLOE/) KLOEK A P.  
 PA (DAVI/) DAVILA-APONTE J A.  
 PA (HRES/) HRESKO M C.  
 PA (MCLA/) MCLAIRD M B.  
 PA (ZENT/) ZENTELLA R.  
 PA (WILL/) WILLIAMS D J.  
 XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;  
 PI Mcclaird MB, Zentella R, Williams DJ;  
 XX  
 DR WPI; 2005-603337/62.  
 DR N-PSDB; AEC02260.



Db 303 FHDVTHVLHLLSYIYHYHAKARDKIPVLGEYKIDTPIPKAMREAKECIIYEP 362  
 QY 364 DADSKHGTYWYHKM 378  
 Db 363 DEDSEHKGFWYHKM 377

## RESULT 11

AAW79743  
 ID AAW79743 standard; protein; 374 AA.

AC AAW79743;

DT 02-FEB-1999 (first entry)

XX Crepis sp. delta-12-epoxygenase.

KW Fatty acid epoxygenase; CrepX gene; delta-12-epoxygenase;

KW mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;  
 KW vegetable oil; oilseed.

OS Crepis sp.

PH Key Location/Qualifiers  
 FT Region 99..104

FT /note= "His-rich region"

FT Region 135..139

FT /note= "His-rich region"

FT Misc-difference 293

FT /note= "encoded by AGN"

FT Misc-difference 305

FT /note= "encoded by GTN"

FT Region 309..313

FT /note= "His-rich region"

XX WO9846762-A1.

XX 22-OCT-1998.

XX 09-APR-1998; 98WO-AU000246.

XX 15-APR-1997; 97AU-00006223.

XX 15-APR-1997; 97AU-00006226.

XX 16-APR-1997; 97US-0043706P.

XX 20-JUN-1997; 97US-0050403P.

XX (CSTR ) COMMONWEALTH SCI & IND RES ORG.

XX (STYM/) STYMNE S.

XX Styenne S, Green A, Singh S, Lenman M;

XX WPI; 1998-568734/48.

XX N-PSDB; AAW63102.

XX New isolated fatty acid epoxygenase gene - used particularly for

PT transforming plants for producing modified oils for use in, e.g.

PT coatings, resins, glues, plastics, surfactants or lubricants.

XX Claim 29; Page 84-86; 150pp; English.

XX This is the amino acid sequence of a novel epoxygenase of a vernolic acid  
 CC -containing Crepis sp. (not crepis palaestina). It was deduced from  
 CC isolated cDNA clone CrepX (see AAW63102). The deduced sequence contains  
 CC His-rich motifs (see AAW79752-54) that are characteristic of mixed  
 CC function monooxygenases, and shows a high degree of homology to a novel  
 CC delta-12-epoxygenase (see AAW79742) of C. palaestina. The invention  
 CC relates generally to novel genetic sequences (see AAW63101-03) encoding  
 CC fatty acid epoxygenases (see AAW79742-44), especially delta-12-  
 CC epoxygenases or mixed function monooxygenases. These provide the means by  
 CC which fatty acid metabolism can be manipulated in e.g. yeast, mould,  
 CC bacteria, insects, birds, mammals and plants (especially oilseed plants  
 CC such as flax), in particular to convert unsaturated fatty acids to

CC epoxygenated fatty acids. The invention includes genetically modified oil  
 CC -accumulating organisms and to the oils derived from them. These oils can  
 CC be used in production of coatings, resins, glues, plastics, surfactants  
 CC or lubricants

XX Sequence 374 AA;

Query Match 72.4%; Score 1510; DB 2; Length 374;

Best Local Similarity 70.4%; Pred. No. 1.8e-153;

Matches 261; Conservative 50; Mismatches 56; Indels 4; Gaps 2;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVVQDLIIITFLTYVANTY 67

Db 8 RTSEKSVMERVSVDPTVTFSLDLKQAIPPHCFQSRVIRSSVVVQDLIIAIFYFLANTY 67

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWLGHEGCHHAFSEYQWIDNAVGFVLHALLTP 127

Db 68 IPNLPHPLAYLAWPLVYWFQASVLTGLWLGHEGCHHAYSNTYVDDTVGFIHSFLITP 127

QY 128 YFSWKYSHRKHANSTNSLENEEVYIPRTQSOLRTYSTYEFLDNTPGRILLIIVIMLTGLFP 187

Db 128 YFSWKYSHRNHHSNTSSINDNDENVYIPKSKLK--RIYKLLNNPPGRLLVLVIMLTGLFP 185

QY 188 LYLITNVSGKKYDRFTNHFDPLSPFTERRIQAVALDGLIVAVFYGLKFLVQTKGCGW 247

Db 186 LYLITNVSGKKYDRFANHFDPMSPIFKEREPQVFLSDGLLAVFYGLKAVANKGAAMV 245

QY 248 MCMYGVPIVGLNSFIIVITLHHLSPHYDSTEMWIKGALTITIDRFGLLNRVHDV 307

Db 246 ACMYGVPLVGVTFEVDITFLHHTHQSPPHYDSTEMWIRGALSADIRDFGLNSVFHDV 305

QY 308 THTHVLHLPPYIPIHYHAKASEAIKPLGDYRMIDRTPPFKAMWREAKECIIYEQDADS 367

Db 306 THTHVMHLPSYIPIHYHAKEARDAIKPLGDYRMIDRTPIPKAMWREGRECMIYE--PDS 363

QY 368 KHKGTYWYHKM 378

Db 364 KLKGTYWYHKL 374

RESULT 12

ADR87360

ID ADR87360 standard; protein; 374 AA.

XX ADR87360;

XX 18-NOV-2004 (first entry)

XX Codon optimised hydroxylase/ epoxygenase, SEQ ID 41.

XX Nematocide; plant; 16C monounsaturated fatty acid;

XX 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;

XX fatty acid epoxygenase; fatty hydroxylase; phospholipid:diacylglycerol;

XX acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;

XX hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;

XX nematode.

XX Crepis biennis.

OS Synthetic.

XX WO2004071168-A2.

XX 26-AUG-2004.

XX 04-FEB-2004; 2004WO-US003254.

XX 05-FEB-2003; 2003US-0445293P.

XX (DIVE-) DIVERGENCE INC.

XX Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;

PI Hresko MC, Mc Laird MB, Zentella R;

XX

DR WPI: 2004-634973/61.  
 XX N-PSDB; ADR87351.  
 PT Novel transgenic plant containing DNA construct having nucleic acid  
 PT encoding polypeptide for catalyzing conversion of substrate to  
 PT monounsaturated fatty acid product, useful for controlling nematodes.  
 XX  
 PS Claim 21; SEQ ID NO 41; 180pp; English.  
 XX  
 XX The present invention relates to transgenic plants (I) containing one or  
 CC more DNA constructs. The DNA constructs have a nucleic acid encoding a  
 CC protein effective for catalyzing the conversion of a substrate to a 16C,  
 CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid  
 CC epoxigenase or a fatty hydroxylase, and a regulatory element operably  
 CC linked to the nucleic acid encoding the protein, where the regulatory  
 CC element confers expression in vegetative tissue of the plant. The fatty  
 CC acid epoxigenase or a fatty hydroxylase can be  
 CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol  
 CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty  
 CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in  
 CC a vegetative tissue. The DNA construct of (I) is useful in the production  
 CC of hydroxylases and epoxigenases that controls nematode damage in  
 CC commercially important plant species and so (I) exhibits increased  
 CC resistance to nematodes. (II) provides an effective, environmentally safe  
 CC methods of inhibiting nematode metabolism, growth, viability,  
 CC development, infectivity and/or the nematode life cycle. (I) provides  
 CC season-long nematode control, thus providing labor savings, by reducing  
 CC the need for and frequency of chemical control. The present sequence is  
 CC one such fatty acid epoxigenase and fatty hydroxylase, which has been  
 CC codon optimised for improved plant expression.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 72.1%; Score 1504; DB 8; Length 374;  
 Best Local Similarity 69.0%; Pred. No. 7.9e-153;  
 Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;  
 QY 1 MSDSDDRMKOHMDERAPIDPAPFSLDLKKAIPAHCPRFRSAVSSCYVVDLIITFL 60  
 Db 1 MASSGHSRTSKSVMERVSDVPVPSLSDLKQAIPHCQFQSVIRSSYVVDHLLIAYIF 60  
 QY 61 YTVANTYIPLPPPLVLAWPVWFQSCILTLGLWVLCGHCGHAFSEYQWIDNAGFVL 120  
 Db 61 YFLADKYIPILPAPLAYLAWPLVWFQASILTGLWILGHCGHAFSEYQWVDVDTVGFW 120  
 QY 121 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYFEFLDNTGRIILVI 180  
 Db 121 HSFLLTPFSWKYSHRNHANTSSINDNEVIPTKSKLAL--TYKLLNPPGRLVMI 178  
 QY 181 MLTLGFPYLLTNVSGKDYDRFTNHPDPLSPITERERIQVALSDLGIVAFYGLKFLVQ 240  
 Db 179 MTLGFPYLLTNVSGKDYDRFANHPDPLSPITERERQVALSDLGIVAFYGLKFLVQ 238  
 QY 241 TKGFGVWCMYGVPIVGLNSFIIVITLHHTLSSPHYSTENWTKGALTIDRDFGLL 300  
 Db 239 KKGAAWVACWYGVPMGLGVFTLFDIITLHHTQSSPHYSTENWIRGALSARDRDFGFM 298  
 QY 301 NRVFHDVTHVHLHLPPIPHYHAKASEAIKPILDYRMIDRTPTFFKAMWREACEY 360  
 Db 299 NSVFHDVTHVHMHMFSPHYHAKARDAINIIGDYIMIDRTPTILKALWREACEY 358  
 QY 361 IEQDADSCKGTWYHKM 378  
 Db 359 IE--PDSKRGVYWHKL 374  
 RESULT 13  
 AEC02274  
 ID AEC02274 standard; protein; 374 AA.  
 XX  
 AC AEC02274;  
 XX  
 DT 06-OCT-2005 (first entry)

XX DE Crepis biennis epoxigenase SEQ ID NO.41.  
 XX transgenic plant; anthelmintic; epoxigenase.  
 KW Crepis biennis.  
 OS Synthetic.  
 OS  
 XX US2005172358-A1.  
 PN  
 XX 04-AUG-2005.  
 PD  
 XX 04-AUG-2004; 2004US-00912534.  
 XX  
 PF 04-FEB-2004; 2004US-00772227.  
 PR  
 XX (VERB/) VERBSKY M L.  
 PA (BAUB/) BAUBLITE C.  
 PA (KLOE/) KLOEK A P.  
 PA (DAVI/) DAVILA-APONTE J A.  
 PA (HRES/) HRESKO M C.  
 PA (MCLA/) MCLAIRD M B.  
 PA (ZENT/) ZENTELLA R.  
 PA (WILL/) WILLIAMS D J.  
 XX Verbsky ML, Baublite C, Kloeck AP, Davila-Aponte JA, Hresko MC;  
 PI Mcclaird MB, Zentella R, Williams DJ;  
 XX WPI: 2005-603337/62.  
 DR N-PSDB; AEC02265.  
 DR  
 XX New transgenic plant having a DNA construct comprising a nucleic acid  
 PT encoding a protein for catalyzing the conversion of a substrate to a C16,  
 PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
 PT anthelmintic compounds.  
 PT  
 XX Claim 21; SEQ ID NO 41; 130pp; English.  
 PS  
 XX The invention relates to a transgenic plant containing at least one DNA  
 CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
 CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
 CC monounsaturated fatty acid product; and (b) a regulatory element operably  
 CC linked to the nucleic acid encoding the polypeptide and conferring  
 CC expression in a vegetative tissue of the plant. Also described: (1) a  
 CC method of making a transgenic plant; (2) an isolated nucleic acid  
 CC comprising the nucleotide sequence; (3) a recombinant nucleic acid  
 CC construct comprising at least one regulatory element that confers  
 CC expression in a vegetative tissue of a plant; and (4) a method of  
 CC screening a transgenic plant for anthelmintic activity. The transgenic  
 CC plant is useful in preparing compounds having anthelmintic activity. The  
 CC present sequence represents an epoxigenase which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 72.1%; Score 1504; DB 9; Length 374;  
 Best Local Similarity 69.0%; Pred. No. 7.9e-153;  
 Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;  
 QY 1 MSDSDDRMKOHMDERAPIDPAPFSLDLKKAIPAHCPRFRSAVSSCYVVDLIITFL 60  
 Db 1 MASSGHSRTSKSVMERVSDVPVPSLSDLKQAIPHCQFQSVIRSSYVVDHLLIAYIF 60  
 QY 61 YTVANTYIPLPPPLVLAWPVWFQSCILTLGLWVLCGHCGHAFSEYQWIDNAGFVL 120  
 Db 61 YFLADKYIPILPAPLAYLAWPLVWFQASILTGLWILGHCGHAFSEYQWVDVDTVGFW 120  
 QY 121 HSAALTPTFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYFEFLDNTGRIILVI 180  
 Db 121 HSFLLTPFSWKYSHRNHANTSSINDNEVIPTKSKLAL--TYKLLNPPGRLVMI 178  
 QY 181 MLTLGFPYLLTNVSGKDYDRFTNHPDPLSPITERERIQVALSDLGIVAFYGLKFLVQ 240  
 Db 179 MTLGFPYLLTNVSGKDYDRFANHPDPLSPITERERQVALSDLGIVAFYGLKFLVQ 238  
 QY 241 TKGFGVWCMYGVPIVGLNSFIIVITLHHTLSSPHYSTENWTKGALTIDRDFGLL 300  
 Db 239 KKGAAWVACWYGVPMGLGVFTLFDIITLHHTQSSPHYSTENWIRGALSARDRDFGFM 298  
 QY 301 NRVFHDVTHVHLHLPPIPHYHAKASEAIKPILDYRMIDRTPTFFKAMWREACEY 360  
 Db 299 NSVFHDVTHVHMHMFSPHYHAKARDAINIIGDYIMIDRTPTILKALWREACEY 358  
 QY 361 IEQDADSCKGTWYHKM 378  
 Db 359 IE--PDSKRGVYWHKL 374

Db 179 MFTLGFPYLLTNISGKKYDRFANHPDMSPIPKERERFQVLLSDGLGLAVFYGIKVA 238  
Qy 241 TKGFGWVMCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTEWNIKALTITDRDFGLL 300  
Db 239 KKAANWACMYGVPMGLGVFTLFDIITYLHHTHQSPPHYDSTEWNIWIRGALSADRDFGFM 298  
Qy 301 NRVDHVTHTVHLHLPYIIPHYHAKSEAKPTLGDYRMDTRTPPKAMWREAKECIY 360  
Db 299 NSVPHDVHTHVMHMFYSIIPHYHAKSEARDAINTIIGDYIMDRTPILKALWREAKECMY 358  
Qy 361 IEQADSKHKGTYYWYHKM 378  
Db 359 IE--PDSKRGVYWHKL 374

RESULT 14  
AEC02370  
ID AEC02370 standard; protein; 374 AA.  
XX AEC02370;  
AC AEC02370;  
DT 06-OCT-2005 (first entry)  
XX 06-OCT-2005 (first entry)  
XX Crepis biennis epoxigenase SEQ ID NO:137.  
XX Crepis biennis epoxigenase.  
XX Crepis biennis.  
XX US2005172358-A1.  
XX 04-AUG-2005.  
XX 04-AUG-2004; 2004US-00912534.  
XX 04-FEB-2004; 2004US-00772227.  
XX (VERB/) VERBSKY M L.  
XX (BAUB/) BAUBLITE C.  
XX (KLOE/) KLOEK A P.  
XX (DAVI/) DAVILA-APONTE J A.  
XX (HRES/) HRESKO M C.  
XX (MCLA/) MCLAIRD M B.  
XX (ZENT/) ZENTELLA R.  
XX (WILL/) WILLIAMS D J.  
XX Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;  
XX Mclaird MB, Zentella R, Williams DJ;  
XX WPI; 2005-603337/62.  
XX N-PSDB; AEC02365.  
XX New transgenic plant having a DNA construct comprising a nucleic acid  
XX encoding a protein for catalyzing the conversion of a substrate to a C16,  
XX C18 or C20 monounsaturated fatty acid product, useful in preparing  
XX anthelmintic compounds.  
XX Claim 21; SEQ ID NO 137; 130pp; English.  
XX The invention relates to a transgenic plant containing at least one DNA  
XX construct comprising: (a) a nucleic acid encoding a polypeptide effective  
XX for catalyzing the conversion of a substrate to a C16, C18, or C20  
XX monounsaturated fatty acid product; and (b) a regulatory element operably  
XX linked to the nucleic acid encoding the polypeptide and conferring  
XX expression in a vegetative tissue of the plant. Also described: (1) a  
XX method of making a transgenic plant; (2) an isolated nucleic acid  
XX comprising the nucleotide sequence; (3) a recombinant nucleic acid  
XX construct comprising at least one regulatory element that confers  
XX expression in a vegetative tissue of a plant; and (4) a method of  
XX screening a transgenic plant for anthelmintic activity. The transgenic  
XX plant is useful in preparing compounds having anthelmintic activity. The  
XX present sequence represents an epoxigenase which is used in the  
XX exemplification of the present invention.

XX Sequence 374 AA;  
Qy Query Match 71.9%; Score 1499; DB 9; Length 374;  
Best Local Similarity 68.8%; Pred. No. 2.7e-152;  
Matches 260; Conservative 51; Mismatches 63; Indels 4; Gaps 2;  
Qy 1 MSDSYDMDKDHMDERAPDPAPFSLDLKKAIPAHCFERSAYMSSCYVVDLIITFL 60  
Db 1 MASSGHRTSKKSYMERVSVDVPFSLDLKQAIPPHCFQKRSVIRSSYVVDHIIATIF 60  
Qy 61 YTVANTYIPHLPPPLVYLAWPVYWFQSCILTLGLWLGHECHGHAFFSEYQWIDNAVGFL 120  
Db 61 YFLADKYIPILPAPLAYLAWPVYWFQSCILTLGLWLGHECHGHAFFSEHQAQVDDTVGFMV 120  
Qy 121 HSALLTFYFWMKYSHRKHANTNSLENEEYVYPTQSLRTYSTYEFIDNTPGRILILVI 180  
Db 121 HSFLLTPTFWMKYSHRNHANTSSIDNDEVYIPKSKKLAL--TYKLINNPGRLLVMVI 178  
Qy 181 MLTLGFPYLLTNISGKKYDRFANHPDMSPIPKERERFQVLLSDGLGLAVFYGIKVA 240  
Db 179 MFTLGFPYLLTNISGKKYDRFANHPDMSPIPKERERFQVLLSDGLGLAVFYGIKVA 238  
Qy 241 TKGFGWVMCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTEWNIKALTITDRDFGLL 300  
Db 239 KKAANWACMYGVPMGLGVFTLFDIITYLHHTHQSPPHYDSTEWNIWIRGALSADRDFGFM 298  
Qy 301 NRVDHVTHTVHLHLPYIIPHYHAKSEAKPTLGDYRMDTRTPPKAMWREAKECIY 360  
Db 299 NSVPHDVHTHVMHMFYSIIPHYHAKSEARDAINTIIGDYIMDRTPILKALWREAKECMY 358  
Qy 361 IEQADSKHKGTYYWYHKM 378  
Db 359 IE--PDSKRGVYWHKL 374

RESULT 15  
ADR87337  
ID ADR87337 standard; protein; 374 AA.  
XX ADR87337;  
XX 18-NOV-2004 (first entry)  
XX Hydroxylase/ epoxigenase, SEQ ID 18.  
XX Nematocide; Plant; 16C monounsaturated fatty acid;  
XX 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;  
XX fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;  
XX acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;  
XX hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;  
XX nematode.  
XX Crepis biennis.  
XX OS  
XX WO2004071168-A2.  
XX PD  
XX 26-AUG-2004.  
XX 04-FEB-2004; 2004WO-US003254.  
XX 05-FEB-2003; 2003US-0445293P.  
XX (DIVE-) DIVERGENCE INC.  
XX Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;  
XX Hresko MC, Mclaird MB, Zentella R;  
XX WPI; 2004-634973/61.  
XX N-PSDB; ADR87325.  
XX Novel transgenic plant containing DNA construct having nucleic acid  
XX encoding polypeptide for catalyzing conversion of substrate to

monounsaturated fatty acid product, useful for controlling nematodes.

Claim 21; SEQ ID NO 18; 180pp; English.

The present invention relates to transgenic plants (I) containing one or more DNA constructs. The DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid epoxigenase or a fatty hydroxylase, and a regulatory element operably linked to the nucleic acid encoding the protein, where the regulatory element confers expression in vegetative tissue of the plant. The fatty acid epoxigenase or a fatty hydroxylase can be a phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in a vegetative tissue. The DNA construct of (I) is useful in the production of hydroxylases and epoxigenases that controls nematode damage in commercially important plant species and so (I) exhibits increased resistance to nematodes. (II) provides an effective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, development, infectivity and/or the nematode life cycle. (I) provides season-long nematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is one such fatty acid epoxigenase and fatty hydroxylase used to illustrate the invention.

Sequence 374 AA:

[illegible]

Search completed: September 22, 2006, 19:38:16

Job time : 201 secs

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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:56:22 ; Search time 34 Seconds  
(without alignments)  
791.157 Million cell updates/sec

Title: US-10-622-774-2

Perfect score: 2086

Sequence: 1 MSDSVDRMKDHMDERAPI.....IYEQADSKHGKTYWHQM 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 260401 seqs, 71162236 residues

Total number of hits satisfying chosen parameters: 260401

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New;

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pap.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description                              |
|------------|--------|-------------|--------|-------|--|
| 1          | 1263   | 60.5        | 383    | 7     | US-11-056-355B-52712 Sequence 52712, A   |
| 2          | 1215   | 58.2        | 377    | 7     | US-11-056-355B-39929 Sequence 39929, A   |
| 3          | 1215   | 58.2        | 377    | 7     | US-11-056-355B-42537 Sequence 42537, A   |
| 4          | 1215   | 58.2        | 377    | 7     | US-11-056-355B-75575 Sequence 75575, A   |
| 5          | 1215   | 58.2        | 377    | 7     | US-11-056-355B-98547 Sequence 98547, A   |
| 6          | 1215   | 58.2        | 377    | 7     | US-11-056-355B-109786 Sequence 109786, A |
| 7          | 1215   | 58.2        | 383    | 7     | US-11-058-746-6 Sequence 6, Appli        |
| 8          | 1215   | 58.2        | 383    | 7     | US-11-056-355B-39928 Sequence 39928, A   |
| 9          | 1215   | 58.2        | 383    | 7     | US-11-056-355B-42536 Sequence 42536, A   |
| 10         | 1215   | 58.2        | 383    | 7     | US-11-056-355B-75574 Sequence 75574, A   |
| 11         | 1215   | 58.2        | 383    | 7     | US-11-056-355B-98546 Sequence 98546, A   |
| 12         | 1215   | 58.2        | 383    | 7     | US-11-056-355B-109785 Sequence 109785, A |
| 13         | 1214   | 58.2        | 377    | 7     | US-11-056-355B-28876 Sequence 28876, A   |
| 14         | 1214   | 58.2        | 377    | 7     | US-11-056-355B-32466 Sequence 32466, A   |
| 15         | 1214   | 58.2        | 383    | 7     | US-11-056-355B-28875 Sequence 28875, A   |
| 16         | 1214   | 58.2        | 383    | 7     | US-11-056-355B-32465 Sequence 32465, A   |
| 17         | 1205.5 | 57.8        | 384    | 7     | US-11-340-318-6 Sequence 6, Appli        |
| 18         | 1192   | 57.1        | 387    | 7     | US-11-058-746-5 Sequence 5, Appli        |
| 19         | 1191.5 | 57.1        | 384    | 7     | US-11-340-318-2 Sequence 2, Appli        |
| 20         | 1187.5 | 56.9        | 384    | 7     | US-11-340-318-4 Sequence 4, Appli        |
| 21         | 1186.5 | 56.9        | 384    | 7     | US-11-058-746-4 Sequence 4, Appli        |
| 22         | 1146   | 54.9        | 384    | 7     | US-11-058-746-7 Sequence 7, Appli        |
| 23         | 1137   | 54.5        | 390    | 6     | US-10-449-902-48623 Sequence 48623, A    |
| 24         | 1133   | 54.3        | 388    | 6     | US-10-449-902-43123 Sequence 43123, A    |
| 25         | 1127   | 54.0        | 381    | 6     | US-10-953-349-28921 Sequence 28921, A    |

RESULT 1

US-11-056-355B-52712  
; Sequence 52712, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 52712  
; LENGTH: 383  
; TYPE: prt  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(383)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177299  
US-11-056-355B-52712

ALIGNMENTS

|    |        |      |     |   |                      |                    |
|----|--------|------|-----|---|----------------------|--------------------|
| 26 | 1127   | 54.0 | 387 | 6 | US-10-953-349-28920  | Sequence 28920, A  |
| 27 | 1124   | 53.9 | 386 | 6 | US-10-953-349-38515  | Sequence 38515, A  |
| 28 | 1124   | 53.9 | 386 | 7 | US-11-056-355B-1518  | Sequence 1518, Ap  |
| 29 | 1124   | 53.9 | 386 | 7 | US-11-056-355B-5995  | Sequence 5995, Ap  |
| 30 | 1124   | 53.9 | 386 | 7 | US-11-056-355B-15295 | Sequence 15295, A  |
| 31 | 1124   | 53.9 | 392 | 6 | US-10-953-349-38514  | Sequence 38514, A  |
| 32 | 1124   | 53.9 | 392 | 7 | US-11-056-355B-1517  | Sequence 1517, Ap  |
| 33 | 1124   | 53.9 | 392 | 7 | US-11-056-355B-5994  | Sequence 5994, Ap  |
| 34 | 1124   | 53.9 | 392 | 7 | US-11-056-355B-15294 | Sequence 15294, A  |
| 35 | 1124   | 53.9 | 456 | 6 | US-10-953-349-38513  | Sequence 38513, A  |
| 36 | 1124   | 53.9 | 456 | 7 | US-11-056-355B-1516  | Sequence 1516, Ap  |
| 37 | 1124   | 53.9 | 456 | 7 | US-11-056-355B-5993  | Sequence 5993, Ap  |
| 38 | 1124   | 53.9 | 456 | 7 | US-11-056-355B-15293 | Sequence 15293, A  |
| 39 | 1114.5 | 53.4 | 362 | 6 | US-10-449-902-36480  | Sequence 36480, A  |
| 40 | 1082   | 51.9 | 350 | 7 | US-11-056-355B-36367 | Sequence 36367, A  |
| 41 | 1082   | 51.9 | 356 | 7 | US-11-056-355B-36366 | Sequence 36366, A  |
| 42 | 1058   | 50.7 | 372 | 7 | US-11-058-746-10     | Sequence 10, Appli |
| 43 | 944.5  | 45.3 | 302 | 7 | US-11-058-746-9      | Sequence 9, Appli  |
| 44 | 934    | 44.8 | 288 | 6 | US-10-953-349-28922  | Sequence 28922, A  |
| 45 | 897    | 43.0 | 309 | 7 | US-11-058-746-8      | Sequence 8, Appli  |

QY 307 VTHVHLHLPYIPHYHAKASEAIKPILDGYRMDTRTPFKAMWREAKECIYEQDAD 366  
Db 311 ITDTHVAHHLFSTMPHYHAMEATKAIPKILGEYRFDTPFVKAMWREARECIYVDPQS 370  
QY 367 SKHKGTYWYH 376  
Db 371 TESKGVFWYN 380

## RESULT 2

US-11-056-355B-39929  
; Sequence 39929, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 39929  
; LENGTH: 377  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(377)  
; OTHER INFORMATION: Ceres Seq. ID no. 12370301  
US-11-056-355B-39929

Query Match 58.2%; Score 1215; DB 7; Length 377;  
Best Local Similarity 55.6%; Pred. No. 1.8e-103;  
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;  
QY 8 RMKDMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVVDLITITFLLYTVANTY 67  
Db 8 KKSETDTTKRVPCPKPPFSGDLKKAIPPHCFKRSIPRSFSLISDIIIIASCIFYVATNY 67  
QY 68 IPHLPPPLVYLAWPYVWFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGFVLSALLTP 127  
Db 68 FSLLPQPLSYLAWPLYWACQCGVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLVLP 127  
QY 128 YFSWKYSHRKHANTNSLENEBEVYIPRTQSOLRTYSTYEFLDNTPGRIILIVIMLTGFP 187  
Db 128 YFSWKYSHRHRHSNTGSLERDEVFPVKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 185  
QY 188 LYLNTNVSCKYDRFTNHFDPISPIFTRERIRIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247  
Db 186 LYLAFNVSGRPYDGFACHFFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAAGQWASM 245  
QY 248 MCMYGVPIVGLNSFIIVITLHHTLSSPHYDSTENWIKGALTITIDRDFGLLNRFHDV 307  
Db 246 ICLYGVPLLIIVNAFLVLTIVLQHTHPSLPHYDSEWDWLRGALATVDRDYGILNKVFHNI 305  
QY 308 THTVHLHLPYIPHYHAKASEAIKPILDGYRMDTRTPFKAMWREAKECIYEQDADS 367  
Db 306 TDTVAHHLFSTMPHYNAMEATKAIPKILGDYIQFDGTPWYVAMYREAKECIYVDPREG 365  
QY 368 KHKGTYWYH 376  
Db 366 DKGGVYWYN 374

## RESULT 3

US-11-056-355B-42537  
; Sequence 42537, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 42537  
; LENGTH: 377  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(377)  
; OTHER INFORMATION: Ceres Seq. ID no. 12337752  
US-11-056-355B-42537

Query Match 58.2%; Score 1215; DB 7; Length 377;  
Best Local Similarity 55.6%; Pred. No. 1.8e-103;  
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;  
QY 8 RMKDMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVVDLITITFLLYTVANTY 67  
Db 8 KKSETDTTKRVPCPKPPFSGDLKKAIPPHCFKRSIPRSFSLISDIIIIASCIFYVATNY 67  
QY 68 IPHLPPPLVYLAWPYVWFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGFVLSALLTP 127  
Db 68 FSLLPQPLSYLAWPLYWACQCGVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLVLP 127  
QY 128 YFSWKYSHRKHANTNSLENEBEVYIPRTQSOLRTYSTYEFLDNTPGRIILIVIMLTGFP 187  
Db 128 YFSWKYSHRHRHSNTGSLERDEVFPVKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 185  
QY 188 LYLNTNVSCKYDRFTNHFDPISPIFTRERIRIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247  
Db 186 LYLAFNVSGRPYDGFACHFFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAAGQWASM 245  
QY 248 MCMYGVPIVGLNSFIIVITLHHTLSSPHYDSTENWIKGALTITIDRDFGLLNRFHDV 307  
Db 246 ICLYGVPLLIIVNAFLVLTIVLQHTHPSLPHYDSEWDWLRGALATVDRDYGILNKVFHNI 305  
QY 308 THTVHLHLPYIPHYHAKASEAIKPILDGYRMDTRTPFKAMWREAKECIYEQDADS 367  
Db 306 TDTVAHHLFSTMPHYNAMEATKAIPKILGDYIQFDGTPWYVAMYREAKECIYVDPREG 365  
QY 368 KHKGTYWYH 376  
Db 366 DKGGVYWYN 374

## RESULT 4

US-11-056-355B-75575  
; Sequence 75575, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 75575  
; LENGTH: 377  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:

|   |     |  |     |
|---|-----|--|-----|
| Db  | 68  | FSLLPQPLSYLAWPLYWACQCVLTGLTWIAHECGHAFSDYQWLDDTDTVGLIFHSLFLVP | 127 |
| Qy  | 128 | YFSWKYSHRKHANTNSLENEEVIPRTQSOLRTYSTYEFELNDTPGRLILIVMLTLGFP   | 187 |
| Db  | 128 | YFSWKYSHRHRHSNTGSLDERDEVFPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP   | 185 |
| Qy  | 188 | LYLLTNVSGKKYDRFTNHFDPPLSPFTERRERIOVALSDLGIVAFYGLKFLVQTKGFGWV | 247 |
| Db  | 186 | LYLAFNVSGRPYDGFACHFFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAQGMASW  | 245 |
| Qy  | 248 | MCMYGVPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLNRFVHDV   | 307 |
| Db  | 246 | ICLYGVPLLIWNAFLVLTLYLQHTHPSLPHYDSEMDWLRGALATVDRDYGILNKVFHNI  | 305 |
| Qy  | 308 | THTHVLHLFPYIPHYHAKESAIAKPILDGYRMIDRTPFFKAMWREAKECIIYEQADS    | 367 |
| Db  | 306 | TDTVAHHLFSTMPHYNAMEATKAIPILGDYQYQDGTWPYVAMYREAKECIYVEPDREG   | 365 |
| Qy  | 368 | KHKGTYYWH 376  |     |
| Db  | 366 | DKKGVYWN 374   |     |
| RESULT 6  |     |  |     |
| US-11-056-355B-109786   |     |  |     |
| ; Sequence 109786, Application US/11056355B                               |     |  |     |
| ; Publication No. US20060150283A1   |     |  |     |
| ; GENERAL INFORMATION:  |     |  |     |
| ; APPLICANT: Brover, Vyacheslav   |     |  |     |
| ; APPLICANT: Alexandrov, Nikolai  |     |  |     |
| ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding |     |  |     |
| ; TITLE OF INVENTION: Polypeptides Encoded Thereby                        |     |  |     |
| ; FILE REFERENCE: 2750-1590PUS2   |     |  |     |
| ; CURRENT APPLICATION NUMBER: US/11/056,355B                              |     |  |     |
| ; CURRENT FILING DATE: 2005-02-14   |     |  |     |
| ; PRIOR APPLICATION NUMBER: 60/544,190                                    |     |  |     |
| ; PRIOR FILING DATE: 2004-02-13   |     |  |     |
| ; NUMBER OF SEQ ID NOS: 119966  |     |  |     |
| ; SEQ ID NO 109786  |     |  |     |
| ; LENGTH: 377   |     |  |     |
| ; TYPE: prt   |     |  |     |
| ; ORGANISM: Arabidopsis thaliana  |     |  |     |
| ; FEATURE:  |     |  |     |
| ; NAME/KEY: peptide   |     |  |     |
| ; LOCATION: (1)..(377)  |     |  |     |
| ; OTHER INFORMATION: Ceres Seq. ID no. 13600978                           |     |  |     |
| US-11-056-355B-109786   |     |  |     |
| Query Match 58.2%; Score 1215; DB 7; Length 377;                          |     |  |     |
| Best Local Similarity 55.6%; Pred. No. 1.8e-103;                          |     |  |     |
| Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;            |     |  |     |
| Qy  | 8   | RMKDHDMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVVDLIITFLLYTVANTY    | 67  |
| Db  | 8   | KKSETDTTKRVPCEKPPFVSGDLKKAIPHCFKRSIPRFSYLSIDIIASCFFYVATNY    | 67  |
| Qy  | 68  | IPHLPPPLVYLAWPVYWFQSCILTLGLWVLCHECGHAFSEYQWIDNAGFVLHSLALTP   | 127 |
| Db  | 68  | FSLLPQPLSYLAWPLYWACQCVLTGLTWIAHECGHAFSDYQWLDDTDTVGLIFHSLFLVP | 127 |
| Qy  | 128 | YFSWKYSHRKHANTNSLENEEVIPRTQSOLRTYSTYEFELNDTPGRLILIVMLTLGFP   | 187 |
| Db  | 128 | YFSWKYSHRHRHSNTGSLDERDEVFPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP   | 185 |
| Qy  | 188 | LYLLTNVSGKKYDRFTNHFDPPLSPFTERRERIOVALSDLGIVAFYGLKFLVQTKGFGWV | 247 |
| Db  | 186 | LYLAFNVSGRPYDGFACHFFPNAPYNDRELRQIYLS DAGILAVCFGLYRYAAQGMASW  | 245 |
| Qy  | 248 | MCMYGVPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLNRFVHDV   | 307 |
| Db  | 246 | ICLYGVPLLIWNAFLVLTLYLQHTHPSLPHYDSEMDWLRGALATVDRDYGILNKVFHNI  | 305 |
| Qy  | 308 | THTHVLHLFPYIPHYHAKESAIAKPILDGYRMIDRTPFFKAMWREAKECIIYEQADS    | 367 |
| Db  | 306 | TDTVAHHLFSTMPHYNAMEATKAIPILGDYQYQDGTWPYVAMYREAKECIYVEPDREG   | 365 |
| Qy  | 368 | KHKGTYYWH 376  |     |
| Db  | 366 | DKKGVYWN 374   |     |
| RESULT 5  |     |  |     |
| US-11-056-355B-98547  |     |  |     |
| ; Sequence 98547, Application US/11056355B                                |     |  |     |
| ; Publication No. US20060150283A1   |     |  |     |
| ; GENERAL INFORMATION:  |     |  |     |
| ; APPLICANT: Brover, Vyacheslav   |     |  |     |
| ; APPLICANT: Alexandrov, Nikolai  |     |  |     |
| ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding |     |  |     |
| ; TITLE OF INVENTION: Polypeptides Encoded Thereby                        |     |  |     |
| ; FILE REFERENCE: 2750-1590PUS2   |     |  |     |
| ; CURRENT APPLICATION NUMBER: US/11/056,355B                              |     |  |     |
| ; CURRENT FILING DATE: 2005-02-14   |     |  |     |
| ; PRIOR APPLICATION NUMBER: 60/544,190                                    |     |  |     |
| ; PRIOR FILING DATE: 2004-02-13   |     |  |     |
| ; NUMBER OF SEQ ID NOS: 119966  |     |  |     |
| ; SEQ ID NO 98547   |     |  |     |
|   |     |  |     |

Db 306 TDTHVAHLFSTMPHYNAMEATKAIKPILDGYQDGTPTWYAMYREAKECIYVEPDREG 365  
QY 368 KHKGTYWYH 376  
Db 366 DKKGYYWYN 374

RESULT 7  
US-11-058-746-6  
; Sequence 6, Application US/11058746  
; Publication No. US20060101543A1  
; GENERAL INFORMATION:  
; APPLICANT: Somerville, Chris  
; APPLICANT: Broun, Pierre  
; APPLICANT: Van de Loo, Frank  
; APPLICANT: Boddupalli, Sekhar S  
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 56100-5022-12  
; CURRENT APPLICATION NUMBER: US/11/058,746  
; CURRENT FILING DATE: 2005-02-16  
; PRIOR APPLICATION NUMBER: US 08/597,313  
; PRIOR FILING DATE: 1996-02-06  
; PRIOR APPLICATION NUMBER: US 08/530,862  
; PRIOR FILING DATE: 1995-09-20  
; PRIOR APPLICATION NUMBER: US 08/320,982  
; PRIOR FILING DATE: 1994-10-11  
; PRIOR APPLICATION NUMBER: US 08/314,596  
; PRIOR FILING DATE: 1994-09-26  
; PRIOR APPLICATION NUMBER: PCT/US95/11855  
; PRIOR FILING DATE: 1995-09-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-058-746-6

Query Match 58.2%; Score 1215; DB 7; Length 383;  
Best Local Similarity 55.6%; Pred. No. 1.9e-103;  
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;  
QY 8 RMDKDHMERAPIDPAPFSLDLKKAIPAHCFFRSVAVSSCYVVDLIITFLTYVANTY 67  
Db 14 KKSETDTTKRVPCCKPFPFSGDLKKAIPHCFFKRSIPRSFSLISDIIIIASCFFYVATNY 73  
QY 68 IPHLPPLVYLAWPYWFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGVLSALLTP 127  
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDLDTVGLIFHSFLVLP 133  
QY 128 YFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYEFDLNTPGRILILVIMLTGFP 187  
Db 134 YFSWKYSHRRHHSNTGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 191  
QY 188 LYLTVNSGKGYDRFTNHFDPSPIFTERERIQVALSDLGIVAVFYGLKPLVQTKGFOW 247  
Db 192 LYLAFNVSGRPYDGFACHPFPNAPYNDRLRQIYLS DAGILAVCFGLYRYAAAGQWASM 251  
QY 248 MCYGVPGVIGLNSPIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLLNRFVHDV 307  
Db 252 ICYGVPLLIWNAFLVLTQLHTPSLPHYDSSDMDLWLRGALATVDRDYGLNKVFHNI 311  
QY 308 THTHVHLHFPYIPHYHAKASEAKPILDGYRMDTRTPPFKAMWREAKECIYEQDADS 367  
Db 312 TDTHVAHLFSTMPHYNAMEATKAIKPILDGYQDGTPTWYAMYREAKECIYVEPDREG 371  
QY 368 KHKGTYWYH 376  
Db 372 DKKGYYWYN 380

RESULT 8  
US-11-056-355B-39928  
; Sequence 39928, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(383)  
; OTHER INFORMATION: Ceres Seq. ID no. 12370300  
US-11-056-355B-39928

Query Match 58.2%; Score 1215; DB 7; Length 383;  
Best Local Similarity 55.6%; Pred. No. 1.9e-103;  
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;  
QY 8 RMDKDHMERAPIDPAPFSLDLKKAIPAHCFFRSVAVSSCYVVDLIITFLTYVANTY 67  
Db 14 KKSETDTTKRVPCCKPFPFSGDLKKAIPHCFFKRSIPRSFSLISDIIIIASCFFYVATNY 73  
QY 68 IPHLPPLVYLAWPYWFCQSCILTLGLWLGHECGHAFSEYQWIDNAVGVLSALLTP 127  
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDLDTVGLIFHSFLVLP 133  
QY 128 YFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTYEFDLNTPGRILILVIMLTGFP 187  
Db 134 YFSWKYSHRRHHSNTGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 191  
QY 188 LYLTVNSGKGYDRFTNHFDPSPIFTERERIQVALSDLGIVAVFYGLKPLVQTKGFOW 247  
Db 192 LYLAFNVSGRPYDGFACHPFPNAPYNDRLRQIYLS DAGILAVCFGLYRYAAAGQWASM 251  
QY 248 MCYGVPGVIGLNSPIVITYLHHTLSSPHYDSTENWIKGALTITIDRDFGLLNRFVHDV 307  
Db 252 ICYGVPLLIWNAFLVLTQLHTPSLPHYDSSDMDLWLRGALATVDRDYGLNKVFHNI 311  
QY 308 THTHVHLHFPYIPHYHAKASEAKPILDGYRMDTRTPPFKAMWREAKECIYEQDADS 367  
Db 312 TDTHVAHLFSTMPHYNAMEATKAIKPILDGYQDGTPTWYAMYREAKECIYVEPDREG 371  
QY 368 KHKGTYWYH 376  
Db 372 DKKGYYWYN 380

RESULT 9  
US-11-056-355B-42536  
; Sequence 42536, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966

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; SEQ ID NO 42536
; LENGTH: 383
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(383)
; OTHER INFORMATION: Ceres Seq. ID no. 12337751
US-11-056-355B-42536

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCPRKSPRSFSLIISDIILASCFYYATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGFVLHSAALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHFSLLVP 133

QY 128 YFSWKYSHRKHANTNSLENEEVIYIPRTQSQRITSTYFELDNTPGRIILIVIMLTGFP 187
Db 134 YFSWKYSHRHRHSNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRINMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFPFNAPYNDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251

QY 248 MCMYGVPIVGLNSFIIVITYLHHTLSSPHYSTENWIKGALTTIDRDFGLLNRFVHDV 307
Db 252 ICYGVPLLIIVNAFLVLTLYLQTHPSLPHYDSSEMDLWLGALATVDRDYGILNKVFHNI 311

QY 308 THTVHLHLFPYIPHYHAKASEAIKPIIGDYRMIDRTPFFKAMWREAKECIYIEQADS 367
Db 312 TDTHVAHLFSTMPHYNAMEATKAIPILGDYIYQFDGTPWYVAMYREAKECIYVEPDREG 371

QY 368 KHKGTYWYH 376
Db 372 DKKGVTWYN 380

RESULT 11
US-11-056-355B-98546
; Sequence 98546, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98546
; LENGTH: 383
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(383)
; OTHER INFORMATION: Ceres Seq. ID no. 13600977
US-11-056-355B-98546

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCPRKSPRSFSLIISDIILASCFYYATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGFVLHSAALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHFSLLVP 133

QY 128 YFSWKYSHRKHANTNSLENEEVIYIPRTQSQRITSTYFELDNTPGRIILIVIMLTGFP 187
Db 134 YFSWKYSHRHRHSNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRINMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFPFNAPYNDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251

Query Match      58.2%; Score 1215; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92; Indels 2; Gaps 1;

QY 8 RMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDLIIITFLTYTANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLKKAIPHCPRKSPRSFSLIISDIILASCFYYATNY 73

QY 68 IPHLPPLVYLAWPVYWFQSCILTLGLWVLCGECGHAFSEYQWIDNAVGFVLHSAALLTP 127
Db 74 FSLLPQPLSYLAWPLYWACQCVLTGIWVIAHECGHAFSDYQWLDDTVGLIFHFSLLVP 133

QY 128 YFSWKYSHRKHANTNSLENEEVIYIPRTQSQRITSTYFELDNTPGRIILIVIMLTGFP 187
Db 134 YFSWKYSHRHRHSNTGSLERDEVFVFKQSAIKWYGY--LNNPLGRINMLTVQFVLGWP 191

QY 188 LYLLTNVSGKKYDRFTNHFDPISPIFTRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 192 LYLAFNVSGRPYDGFACHFPFNAPYNDRERLQIYLSDAGILAVCFGLYRYAAQAQWASM 251
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; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)-(377)
; OTHER INFORMATION: Ceres Seq. ID no. 12321217
; US-11-056-355B-32466

Query Match      58.2%; Score 1214; DB 7; Length 377;
Best Local Similarity 55.6%; Pred. No. 2.3e-103;
Matches 205; Conservative 69; Mismatches 93; Indels 2; Gaps 1;

QY 8 RMDKDHMDERAPDAPFSLDLKKAIPAHCFPRSAWSSCYVQDLITFLLYTVANTY 67
Db 8 KKSETDTTKRVPCEKPPFSVGLDKKAIPHPCHKRSIPRSFYLSIDIIASCFFYVATNY 67
QY 68 IPHLPPLVYLAWPVYWFQSCILTGLWVLGHCCHHAFSEYQWIDNAVGFVLHSLTLP 127
Db 68 FSLLPQPLSYLAWPLYWACGCVLTGIWVIAHECGHAFSDYQWLDDTIVGLIFHSLFVLP 127
QY 128 YFSWKYSHRKHANTNSLENEEYIIPRTOSQLRTYSTYEFDLNTPGRIILILVIMLTGFP 187
Db 128 YFSWKYSHRHRHNTSGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 185
QY 188 LYLLTNVSGKKYDRFTNHFDPSPITERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 188 LYLLTNVSGKKYDRFTNHFDPSPITERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
QY 192 LYLAFAVNSGRPYDGFACHFPFNAPIYNDRELRQIYLSGAGILAVCFGLYRYAAAGWASM 251
Db 192 LYLAFAVNSGRPYDGFACHFPFNAPIYNDRELRQIYLSGAGILAVCFGLYRYAAAGWASM 251
QY 248 MCMYGPVIGLNSFIIVITLHHTLSSPHYDSTENWIKGALTTIDRDFGLNRPVHDV 307
Db 248 MCMYGPVIGLNSFIIVITLHHTLSSPHYDSTENWIKGALTTIDRDFGLNRPVHDV 307
QY 252 ICYGVPLLVNAFLVLTLYLQHTPSLPHYDSEWDLRGALATVDRDYGILNKVFHNI 311
Db 252 ICYGVPLLVNAFLVLTLYLQHTPSLPHYDSEWDLRGALATVDRDYGILNKVFHNI 311
QY 308 THTHVLHLFPYIPHYHAKESAEAIKPILDGYRMDRTPFFKAMWREAKECIYVEPDADS 367
Db 308 THTHVLHLFPYIPHYHAKESAEAIKPILDGYRMDRTPFFKAMWREAKECIYVEPDADS 367
QY 312 THTHVAHLFSTMPHYNAMEATNAIKPILGDYQPDGTPWYVAMYREAKECIYVEPDREG 371
Db 312 THTHVAHLFSTMPHYNAMEATNAIKPILGDYQPDGTPWYVAMYREAKECIYVEPDREG 371
QY 368 KHKGTYYWH 376
Db 368 KHKGTYYWH 376
QY 372 DKKGVYWN 380
Db 372 DKKGVYWN 380

Search completed: September 22, 2006, 19:59:58
Job time : 35 secs

; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)-(377)
; OTHER INFORMATION: Ceres Seq. ID no. 12321217
; US-11-056-355B-32466

Query Match      58.2%; Score 1214; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 2.3e-103;
Matches 205; Conservative 69; Mismatches 93; Indels 2; Gaps 1;

QY 8 RMDKDHMDERAPDAPFSLDLKKAIPAHCFPRSAWSSCYVQDLITFLLYTVANTY 67
Db 8 KKSETDTTKRVPCEKPPFSVGLDKKAIPHPCHKRSIPRSFYLSIDIIASCFFYVATNY 67
QY 68 IPHLPPLVYLAWPVYWFQSCILTGLWVLGHCCHHAFSEYQWIDNAVGFVLHSLTLP 127
Db 68 FSLLPQPLSYLAWPLYWACGCVLTGIWVIAHECGHAFSDYQWLDDTIVGLIFHSLFVLP 127
QY 128 YFSWKYSHRKHANTNSLENEEYIIPRTOSQLRTYSTYEFDLNTPGRIILILVIMLTGFP 187
Db 128 YFSWKYSHRHRHNTSGSLERDEVFVPKQSAIKWYGY--LNNPLGRIMMLTVQFVLGWP 185
QY 188 LYLLTNVSGKKYDRFTNHFDPSPITERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 188 LYLLTNVSGKKYDRFTNHFDPSPITERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
QY 192 LYLAFAVNSGRPYDGFACHFPFNAPIYNDRELRQIYLSGAGILAVCFGLYRYAAAGWASM 251
Db 192 LYLAFAVNSGRPYDGFACHFPFNAPIYNDRELRQIYLSGAGILAVCFGLYRYAAAGWASM 251
QY 248 MCMYGPVIGLNSFIIVITLHHTLSSPHYDSTENWIKGALTTIDRDFGLNRPVHDV 307
Db 248 MCMYGPVIGLNSFIIVITLHHTLSSPHYDSTENWIKGALTTIDRDFGLNRPVHDV 307
QY 252 ICYGVPLLVNAFLVLTLYLQHTPSLPHYDSEWDLRGALATVDRDYGILNKVFHNI 311
Db 252 ICYGVPLLVNAFLVLTLYLQHTPSLPHYDSEWDLRGALATVDRDYGILNKVFHNI 311
QY 308 THTHVLHLFPYIPHYHAKESAEAIKPILDGYRMDRTPFFKAMWREAKECIYVEPDADS 367
Db 308 THTHVLHLFPYIPHYHAKESAEAIKPILDGYRMDRTPFFKAMWREAKECIYVEPDADS 367
QY 312 THTHVAHLFSTMPHYNAMEATNAIKPILGDYQPDGTPWYVAMYREAKECIYVEPDREG 371
Db 312 THTHVAHLFSTMPHYNAMEATNAIKPILGDYQPDGTPWYVAMYREAKECIYVEPDREG 371
QY 368 KHKGTYYWH 376
Db 368 KHKGTYYWH 376
QY 372 DKKGVYWN 380
Db 372 DKKGVYWN 380

RESULT 15
US-11-056-355B-28875
; Sequence 28875, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 28875
; LENGTH: 383
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)-(383)
; OTHER INFORMATION: Ceres Seq. ID no. 12321216
; US-11-056-355B-28875

Query Match      58.2%; Score 1214; DB 7; Length 383;
Best Local Similarity 55.6%; Pred. No. 2.3e-103;
Matches 205; Conservative 69; Mismatches 93; Indels 2; Gaps 1;

QY 8 RMDKDHMDERAPDAPFSLDLKKAIPAHCFPRSAWSSCYVQDLITFLLYTVANTY 67
Db 14 KKSETDTTKRVPCEKPPFSVGLDKKAIPHPCHKRSIPRSFYLSIDIIASCFFYVATNY 73
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: September 22, 2006, 19:38:36 ; Search time 42 Seconds  
(without alignments)  
865.951 Million cell updates/sec  
Title: US-10-622-774-2  
Perfect score: 2086  
Sequence: 1 MSDSYDRMKDHMDERAPI.....IYIEQDADSKHGTYHYHKM 378  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 80: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID  | Description        |
|------------|--------|-------------|--------|--------|--------------------|
| 1          | 1271   | 60.9        | 383    | T10480 | Delta12 fatty acid |
| 2          | 1240   | 59.4        | 382    | T15042 | omega-6 fatty acid |
| 3          | 1234   | 59.2        | 383    | T07688 | omega-6 desaturase |
| 4          | 1226   | 58.8        | 383    | T10789 | omega-6 desaturase |
| 5          | 1214.5 | 58.2        | 385    | T09880 | omega-6 desaturase |
| 6          | 1203   | 57.7        | 378    | T14269 | Delta12 fatty acid |
| 7          | 1192   | 57.1        | 387    | T09839 | oleate 12-hydroxyl |
| 8          | 1176   | 56.4        | 383    | T15043 | fungal elicitor-in |
| 9          | 1170.5 | 56.1        | 387    | T07687 | omega-6 desaturase |
| 10         | 1090   | 52.3        | 333    | T07009 | omega-6 fatty acid |
| 11         | 907.5  | 43.5        | 376    | JC7871 | stearoyl-CoA 9-des |
| 12         | 640    | 30.7        | 359    | AG2005 | omega-3 fatty acid |
| 13         | 638    | 30.6        | 441    | T03029 | omega-3 fatty acid |
| 14         | 634    | 30.4        | 431    | T07685 | omega-3 fatty acid |
| 15         | 612.5  | 29.4        | 438    | T15039 | omega-3 fatty acid |
| 16         | 611.5  | 29.3        | 460    | T10063 | omega-3 fatty acid |
| 17         | 603    | 28.9        | 398    | T01696 | omega-3 fatty acid |
| 18         | 602.5  | 28.9        | 453    | JQ2339 | omega-3 fatty acid |
| 19         | 601    | 28.8        | 379    | JQ3555 | omega-3 fatty acid |
| 20         | 597.5  | 28.6        | 386    | JQ2335 | omega-3 fatty acid |
| 21         | 594.5  | 28.5        | 381    | T03923 | probable omega-3 f |
| 22         | 594    | 28.5        | 443    | T01697 | omega-3 fatty acid |
| 23         | 593.5  | 28.5        | 446    | JQ2336 | omega-3 fatty acid |
| 24         | 588.5  | 28.2        | 377    | JQ2337 | omega-3 fatty acid |
| 25         | 587.5  | 28.2        | 418    | JC7872 | stearoyl-CoA 9-des |
| 26         | 585    | 28.0        | 380    | T10898 | probable omega-3 f |
| 27         | 583    | 27.9        | 404    | PQ0812 | omega-3 fatty acid |
| 28         | 579.5  | 27.8        | 383    | A44227 | omega-3 fatty acid |
| 29         | 578.5  | 27.7        | 380    | JQ2338 | omega-3 fatty acid |

RESULT 1  
T10480  
Delta12 fatty acid desaturase (EC 1.14.99.-) [imported] - Commerson's wild potato  
C:Species: Solanum commersonii (Commerson's wild potato)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T10480  
R:Consiglio, F.; Amatruda, M.R.; Leone, A.; Costa, A.; Grillo, S.  
Submitted to the EMBL Data Library, November 1995  
A:Reference number: Z17044  
A:Accession: T10480  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-383 <CON>  
A:Cross-references: UNIPROT:Q41305; UNIPARC:UPI0000033AA3; EMBL:X92847; NID:gl054842; PII  
A:Experimental source: clone ScDes D111  
C:Superfamily: fatty acid (acyl-CoA) desaturase  
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

ALIGNMENTS

Query Match 60.9%; Score 1271; DB 2; Length 383;  
Best Local Similarity 58.3%; Pred. No. 2.7e-99;  
Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;

|    |     |   |     |
|----|-----|---|-----|
| QY | 16  | ERAPIDPAPFSLDLKKAIPAHCRRSAVWSSCYVVDLIITFLTYVANTYIPHLPPPL    | 75  |
| DB | 22  | QKVPTSKPFTVGDIKKAIPHCFCQSLRSFSYVVDLILVSIMYVANTYFHLPPSY      | 81  |
| QY | 76  | VYLAWPVWFOQCILTGLWVLGHCCHHAFSEYQWIDNAGFVLHSAALLTPYFSWKYSH   | 135 |
| DB | 82  | CYIAWPIYWCQGCVCCTGIWVNAHCCHHAFSDYQWDDTVGLILHSAALLVPYFSWKYSH | 141 |
| QY | 136 | RKHANTNSLENEEYVIRPTQSOLATYSTYFELDNTGRILILVIMLTGLGFLYLLTNVS  | 195 |
| DB | 142 | RRHNSNTGSLREDFVFPKPSQLGWYSKY--LNNPPGRVLSLTITLTUGWPLYLAFNVS  | 199 |
| QY | 196 | GKKYDRFTNHPDPLSPIFTERERIOVALSDLGIVAFYGLKFLVOTKFGWVWCYGVFV   | 255 |
| DB | 200 | GRPYDRFACHYDPYGIYNNRRLQIFISDAGVLGVCLLYLXIALVKGLAWLCVYGVPL   | 259 |
| QY | 256 | IGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDGLNLRVFDVTHVHLHH     | 315 |
| DB | 260 | LVVNGFLVITLQHTPLSPHYDSTEDWLKALATCDRDYGVLMKVPFHNITDTHVHH     | 319 |
| QY | 316 | LPFYPIHYHAKESAIKPIGDIYRMIDRTFFKAMWEAKECIYEQDADSKHGTYHY      | 375 |
| DB | 320 | LFSTMPHYNAMEATKAVKPLLDGYQFDGTPIYKEMWREAKCLYVKKDESSQGGVFWY   | 379 |

RESULT 2  
T15042  
omega-6 fatty acid desaturase (EC 1.14.99.-) - parsley  
C:Species: Petroselinum crispum (parsley)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

|                       |              |                    |            |             |
|-----------------------|--------------|--------------------|------------|-------------|
| Query Match           | 59.2%        | Score 1234;        | DB 2;      | Length 383; |
| Best Local Similarity | 57.0%        | Pred. No. 3.5e-96; |            |             |
| Matches 211:          | Conservative | 68: Mismatches     | 89: Indels | 2: Gaps     |

A; Experimental source: strain Mammoth

196 GKKYDRFTNHFDP LSP IFT ERER IOALSD LGIVAVFYGLKFLVOTKGF GWMCMYGPV 25

A; EXPERIMENTAL SOURCE: VSTATI MAIINOCII

Db 204 GRPYDRFACHYDYPGPIFSERERQIYADIAGIFATFVLVQATMAKGLAWMRIYGVPL 263  
Qy 256 IGLNSFIIVITLHHTLSSPHYDSTENWIKGALTITDRDGLLNRFVHDVTHVLHH 315  
Db 264 LIVNCFVMIYQLQTHPAIPRYGSSEWDLRGAVTVDRDYGVLNKVFHNIADTHVAH 323  
Qy 316 LPPIPHYHAKASEAIKPIIGDYRMIDRTDTPFKAMWREAKECIYIEODADSKHGTYWY 375  
Db 324 LFATVPYHAMEATKAIPGEYRVYDGTDFYKALWREAKECLFVBPDEGAPTQGVFWY 383  
RESULT 8  
Ti5043  
fungal elicitor-induced protein - parsley  
C:Species: Petroselinum crispum (parsley)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: TJ5043  
R:Kirsch, C.; Hahnbrock, K.; Somssich, I.E.  
Plant Physiol. 115, 283-289, 1997  
A:Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desat  
A:Reference number: Z18274; MUID:97451781; PMID:9306702  
A:Accession: TJ5043  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-383 <KIR>  
A:Cross-references: UNIPROT:O24472; UNIPARC:UPI00000A7AA9; EMBL:U86374; NID:92501791; PI  
C:Genetics:  
A:Gene: ELI12  
C:Superfamily: fatty acid (acyl-CoA) desaturase  
Query Match 56.4%; Score 1176; DB 2; Length 383;  
Best Local Similarity 54.5%; Pred. No. 2.7e-91;  
Matches 205; Conservative 74; Mismatches 93; Indels 4; Gaps 3;  
Qy 1 MSDSDVDRMKDHMDERADIPAPPSLSDLKKAIPAHCFRPSAVSSCYVVDLLITPL 60  
Db 7 MSDPPSGKKTAALAKRAPHBKPPPTIGDLKKAIPAHCFQKSLVTSFYLLIQDLFMAVAL 66  
Qy 61 YTVANTYI-PHLPPLVYLAWPVYWFQSCILTLGLWVLGHECGHAFSEYQWIDNAVGFV 119  
Db 67 FVATNYIDQYLPFPNVMAAYIATVQCVLTGAWVGVGECDDHDAFNSYNWINDLVGLV 126  
Qy 120 LHSALLTPYFNKSHRKHHANTNSLENEEVIPTQQLRTYSTYFELDTNTPGRILLV 179  
Db 127 VHSLLVPYFYSKISHRRHANTQSLNDEVVPRFKSNIRNY--YKLLNPPGKRVLYWL 184  
Qy 180 IMLTLGFPYLLTNVSGKKYDRFTNHPDPLSPIETERIOVALSDLGIVAVFYGLKFLV 239  
Db 185 TTLGLGFPYLLMNFVSGHKYERWTSHYDPHSPLYSDRERKEIIVSDIALLAVIYDLYQLV 244  
Qy 240 QTKGFGWCMYGVPIVGLNSFIIVITLHHTLSSPHYDSTENWIKGALTITDRDGL 299  
Db 245 LAKGFAPVFCVYGGPLLNVGFWLYTLNHTHPSLPYDSTEWDLRGALCTVDYDGI 304  
Qy 300 LNRVPHDVTHVLHLLFPYPHYHAKASEAIKPIIGDYRMIDRTDTPFKAMWREAKECI 359  
Db 305 LNKVPHNYCNHVCVHHIFSMIPHYHGLESTAMKPILGYYQYDGTPTILKAMYREMKCI 364  
Qy 360 YIEQDADSKHGKTYWY 375  
Db 365 YVEKD-EGETKGVYWY 379  
RESULT 9  
T07687  
omega-6 desaturase FAD2-1, microsomal - soybean  
C:Species: Glycine max (soybean)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07687  
R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.  
Plant Physiol. 110, 311-319, 1996  
A:Title: Developmental and growth temperature regulation of two different microsomal om

A:Reference number: Z16095; MUID:9615151506; PMID:8587990  
A:Accession: T07687  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-387 <HEP>  
A:Cross-references: UNIPROT:P48630; UNIPARC:UPI0000033AA4; EMBL:L43920; NID:9904151; PID  
A:Experimental source: seed  
C:Genetics:  
A:Gene: FAD2-1  
C:Function:  
A:Description: involved in production of polyunsaturated lipids; plays a major role in c  
A:Note: strongly expressed in developing seeds  
C:Superfamily: fatty acid (acyl-CoA) desaturase  
Query Match 56.1%; Score 1170.5; DB 2; Length 387;  
Best Local Similarity 54.0%; Pred. No. 7.9e-91;  
Matches 194; Conservative 71; Mismatches 91; Indels 3; Gaps 2;  
Qy 17 RAPIDPAPPSLSDLKKAIPAHCFRPSAVSSCYVVDLLITFLLYTVANTVYIHLPPPLV 76  
Db 28 RVNTEKPPFTVGQKKAIPHCQFQSLTSFSYVVDLSFAFYF-IATTFHLLPPFS 86  
Qy 77 YLAWPVYWFQSCILTLGLWVLGHECGHAFSEYQWIDNAVGFVLHSAALLTPYFSWKYSHR 136  
Db 87 LIAPIYVVLQGCLLTGVWVIAHECGHAFSKYQWVDVVGTLTSHSTLLVPYFSWKISHR 146  
Qy 137 KHANTNSLENEEVIPTQQLRTYSTYFELDTNTPGRILLVIMLTGLGPYLLITNVSG 196  
Db 147 RHHSNTGSLDRDEVFVPKPKSKVAMFSKY--LANNPLGRAVSLVTLTIGWPMYLAFNVS 204  
Qy 197 KYDRFTNHPDPLSPIETERIOVALSDLGIVAVFYGLKFLVQTKGFGWCMYGVYVPI 256  
Db 205 RPYDSPASHHPYAPIYSNRERLLIYSDVALFSVTVSLRVATLKGVLWLLCYGVPL 264  
Qy 257 GLNSFIIVITLHHTLSSPHYDSTENWIKGALTITDRDGLLNRFVHDVTHVLHLL 316  
Db 265 IVNGFLVITLYLQHTHFPALPHYDSSEWDLKALATMDRDYGLNKFVHITDTHVAHLL 324  
Qy 317 PPIPHYHAKASEAIKPIIGDYRMIDRTDTPFKAMWREAKECIYIEODADSKHGKTYWY 375  
Db 325 FSTMPHYHAMEATNAIKPILGYYQYDGTPTFKALWREARECLYVEPDEGTSEKGVYWY 383  
RESULT 10  
T07009  
omega-6 fatty acid desaturase (EC 1.14.99.-) defense-related - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T07009  
R:Gadea, J.; Mayda, E.; Conejero, V.; Vera, P.  
Mol. Plant Microbe Interact. 9, 409-415, 1996  
A:Title: Characterization of defense-related genes ectopically expressed in viroid-infect  
A:Reference number: Z15859; MUID:96252900; PMID:8672818  
A:Accession: T07009  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-333 <GAD>  
A:Cross-references: UNIPROT:Q43500; UNIPARC:UPI00000A4D15; EMBL:X94944; NID:91161567; PI  
A:Experimental source: cultivar Rutgers; leaf  
C:Genetics:  
A:Gene: cev119  
C:Superfamily: fatty acid (acyl-CoA) desaturase  
C:Keywords: oxidoreductase  
Query Match 52.3%; Score 1090; DB 2; Length 333;  
Best Local Similarity 52.5%; Pred. No. 3.9e-84;  
Matches 189; Conservative 55; Mismatches 64; Indels 52; Gaps 3;  
Qy 16 ERAPIDPAPPSLSDLKKAIPAHCFRPSAVSSCYVVDLLITFLLYTVANTVYIHLPPPL 75  
Db 22 ERVPSSKPPFTIGDVKKAIPHCQFQSLTSFSYVVDLSFAFYF-IATTFHLLPPFS 81  
Qy 76 YLAWPVYWFQSCILTLGLWVLGHECGHAFSEYQWIDNAVGFVLHSAALLTPYFSWKYSH 135

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Db 82 RYVAVTYIAQGCVCVTGIWVIGHECGHGFSDYQWVDIVGLIHLHSALLTFYFAWKSH 141
Qy 136 RKHHANTNSLENEEVIPRTQSQLRTYSTVEFLDNTPGRIILIVMLTGLGFLYLLTNVS 195
Db 142 RRHHANTSGLENDIYIPRLKSLR----- 166
Qy 196 GKXYDRFTNHPDPLSPFIFTERERIOVALSDLGIVAVFYGLKFLVQKFGWCMYGVV 255
Db 167 GKXYDRFACHYDPSPISYNNRRLQIYISDVGVATYLLYRVTLTQ----- 213
Qy 256 IGLNSFIIVTYLHTHLSPPHYDSFENWIKGALTITDRDCLNRFVHDVTHTVLHH 315
Db 214 -GLAGFIVLITLMHTHLSPLHYDSSEWHLRGALATVDRDGLAKNVFHNVTDTLH 272
Qy 316 LPYIPPHYHAKASEAIKPIGLDYRMDRTPPFKAMWREAKECIYFEQDADSKHGTYWY 375
Db 273 IFSYISHYHAMEAKKAIPKELGLEYKYDTPILKAMWRTKECIFVEKDKD---KG 329
RESULT 11
JC7871
stearyl-CoA 9-desaturase (EC 1.14.19.1), PAD2 - Chlorella vulgaris
N:Alternate names: acyl-CoA desaturase; delta12 stearyl-CoA desaturase; delta9-desaturase
C:Species: Chlorella vulgaris
C>Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C:Accession: JC7871
R:Suiga, K.; Honjoh, K.; Furuwa, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, Y.;
Biosci. Biotechnol. Biochem. 66, 1334-1327, 2002
A:Title: Two low-temperature-inducible Chlorella genes for delta12 and omega-3 fatty acid
s cerevisiae, and expression of omega-3 fad in Nicotiana tabacum.
A:Reference number: JC7871; MUID:22152188; PMID:12162554
A:Accession: JC7871
A:Molecule type: mRNA
A:Residues: 1-376 <SUG>
A:Cross-references: UNIPROT:QW314; UNIPARC:UPI000008AB54; DDBJ:AB075526
C:Comment: This enzyme is involved in low temperature adaptation, and is also involved in
C:Genetics:
A:Gene: fad2
C:Superfamily: fatty acid (acyl-CoA) desaturase
C:Keywords: oxidoreductase
Query Match 43.5%; Score 907.5; DB 2; Length 376;
Best Local Similarity 45.8%; Pred. No. 1e-68;
Matches 168; Conservative 76; Mismatches 112; Indels 11; Gaps 8;
Qy 17 RAPIDPAP-FSLSDLKKAIPAHCFRRSAVSSCVVQDLIIITFLTYVANTYIPHLPPPL 75
Db 15 RQPVNTKPAFSVSTLRKAIPAHCFRRSAVSSCVVQDLIIITFLTYVANTYIPHLPPPL 73
Qy 76 V--YLA-WPVYWFQSCILTLGLVGHGCHHAFSEVQWIDNAGVFLHSALITPVFSWK 132
Db 74 AVRWLALNPAYWYLAGAVATGIWVIAHCGHQAFSDYQAVNDGVGLVLSLLVPIYSWK 133
Qy 133 YSHRKHANTNSLENEEVIPRTQSQLRTYSTVEFLDNTPGRIILIVMLTGLGFLYLLT 192
Db 134 HSHRRHNTGNVNDKDEVPFPPTREVS--DKWELEQAMPRLVKLFIITLGLWPLYLAF 191
Qy 193 NVSGKKYDR-FTNHPDPLSPFIFTERERIOVALSDLGIVAVFYGLKFLVQKFGWCMY 251
Db 192 NVASRPYKSNWNHFDPMSPFISFKRELVEVAVSDAALVAVLCGLRQLAASFGWMLVKTW 251
Qy 252 GYPVIGLSFIIVTYLHTHLSPPHYDSFENWIKGALTITDRDCLNRFVHDVTHTVH 310
Db 252 LVPYLVNFWLVTITWLQHSHPHLPYHGEWDLRGALTVDVDRDGVGLNSLHHIADT 311
Qy 311 HVLHLFPPIPHYHAKASEAIKPIGLDYRMDRTPPFKAMWREAKECIYFEQDADSKHK 370
Db 312 HVAHLFSPMPHYHAQENTALKPVLGDYRSRPLQLQAIWQDFGSCRYVADTFG--D 369
Qy 371 GTYWHK 377
Db 370 GVLWPK 376
```

## RESULT 12

```
AG2005
omega-3 fatty acid desaturase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004
C:Accession: AG2005
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
R.; Kaneko, T.; Nakamura, Y.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
Nakazaki, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
R.; Kaneko, T.; Nakamura, Y.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KUR>
A:Cross-references: UNIPROT:Q8YWL1; UNIPARC:UPI00000CE141; GB:BA000019; PIDN:BAB77963.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1597
C:Superfamily: fatty acid (acyl-CoA) desaturase
Query Match 30.7%; Score 640; DB 2; Length 359;
Best Local Similarity 36.1%; Pred. No. 3.2e-46;
Matches 122; Conservative 74; Mismatches 122; Indels 20; Gaps 6;
Qy 24 PFSLDLKAIPAHCFRRSAVSSCVVQDLIIITFLTYVANTYIPHLPPPLVYLAWPVY 83
Db 24 PPTLDLKAIPAHCFRRSAVSSCVVQDLIIITFLTYVANTYIPHLPPPLVYLAWPVY 76
Qy 84 WFCQSCILTLGLVGHGCHHAFSEVQWIDNAGVFLHSALITPVFSWKYSHRKHANTN 143
Db 77 WLIOQTMFWALFVGHGCHHAFSEVQWIDNAGVFLHSALITPVFSWKYSHRKHANTN 136
Qy 144 SLENEEVIPRTQSQLRTYSTVEFLDNTPGRIILIVMLTGLGFLYLLTNVSGKKYDR 203
Db 137 NIDNDESWPVTSQVKEMP---LQKIGIYVYVFL---LAYPVYLFKRSNPKE---G 184
Qy 204 NHFDPLSPFIFTERERIOVALSDLGIVAVFYGLKFLVQKFGWCMYGVVIGLSFI 263
Db 185 SHFLPSSSLFKPSEKWDVITSTVLWSCVMGLGFLTYQGMWMLLYKYYAAPYIVFV 244
Qy 264 VTYLHTHLSPPHYDSFENWIKGALTITDRDCLNRFVHDVTHTVHLLFPPIPHY 323
Db 245 LVTFLLHTTEADLPWYRGEDMTLKGAISSIDRNYGLVNHIIHDI-GTHVAHIFLNI 303
Qy 324 HAKEASEAIKPIGLDYRMDRTPPFKAMWREAKECIYI 361
Db 304 NLKATEAIKPMGGEYRKSEBPINWKLWRSVCVSHFV 341
RESULT 13
T03029
omega-3 fatty acid desaturase (EC 1.14.99.-) PAD7 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03029
R:Hamada, T.; Nishuchi, T.; Kodama, H.; Nishimura, M.; Iba, K.
Plant Cell Physiol. 37, 606-611, 1996
A:Title: CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 fatty acid
A:Reference number: Z14828; MUID:96416425; PMID:8819308
A:Accession: T03029
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-441 <HAM>
A:Cross-references: UNIPROT:P93350; UNIPARC:UPI00000A5D90; EMBL:D79979; NID:g1694624; PII
A:Experimental source: cultivar SR1
C:Genetics:
A:Gene: PAD7
C:Superfamily: fatty acid (acyl-CoA) desaturase
C:Keywords: oxidoreductase
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Query Match 30.6%; Score 638; DB 2; Length 441;  
Best Local Similarity 37.9%; Pred. No. 5.9e-46;  
Matches 136; Conservative 62; Mismatches 129; Indels 32; Gaps 10;

QY 19 PIDAPPSSDLKKAIPAHCRRSAVMSVCYVQDLITLITLYTANTYIPLHPLPLVYL 78  
DB 89 PGAPPPFKLSIDKKAIPKHCWVKWPKMSVYVRDVAIVFGL-AAAAAYFNN-----WV 141  
QY 79 AWPVYWFQSCILTLGLWVLCGHHAFSEYQWIDNAVGVFLHSAALLTPYFSWKYSHRKH 138  
DB 142 WPLVYMPAQSMFWALFVLGHDGCHGFSNNHKLNSVGVHILHSSILVPYHGWIRSHRTH 201  
QY 139 HANTNSLENEEYIPRTQSOLRTYSTYFPLNTPGORILILVIMLTGLFPLLYLLTVNSGKK 198  
DB 202 HQNHGHVNDSEWHPIPE-----KIYNSLDLTKKLFRTLPFPLLAYPFYLWGRSPGKK 255  
QY 199 YDRFTNHPDPSIPFTRERIRIOVALSDL--GIVAVFYGLKPLVQTKFGWCMVMYGVVPV 255  
DB 256 ----GSHFDPNSDLFVPSKKVDVMTSLCWTAMAALLVGLSFVM---GPFQVLKLYGIPY 308  
QY 256 IGLNSFIIVTYLHHTLSS--PHYDSTENWIKGALTITDRDGLLNRPVHDTHTHVL 313  
DB 309 WGFVWMLDLVTVLHHGHDDKLPWYRGSEWSYLRGGLTTLDYDYGWNNIHHDI-GTHVI 367  
QY 314 HHLPPYIPIHYHAKESAIAKILGDY-----RMIDRTPF--KAMWREAKECIYIQQDAD 366  
DB 368 HHLFPQIPHYHLVEATEAKPVLGKYKEPKSGPLPFYLLGLVLSKMQDHYVSDTGD 426

RESULT 14  
T07685  
omega-3 fatty acid desaturase (EC 1.14.99.-) - potato  
N/Alternate names: w-3 desaturase  
C/Species: Solanum tuberosum (potato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C/Accession: T07685  
R/Leon, J.  
submitted to the EMBL Data Library, August 1998  
A/Reference number: Z16092  
A/Accession: T07685  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: mRNA  
A/Residues: 1-431 <LEO>  
A/Cross-references: UNIPROT:O82068; UNIPARC:UPI000009E6DD; EMBL:AJ007739; PIDN:CAA07638.  
A/Experimental source: cv. Desiree  
C/Function:  
A/Pathway: fatty acid biosynthesis  
A/Superfamily: fatty acid (acyl-CoA) desaturase  
C/Keywords: oxidoreductase

Query Match 30.4%; Score 634; DB 2; Length 431;  
Best Local Similarity 38.9%; Pred. No. 1.3e-45;  
Matches 132; Conservative 60; Mismatches 121; Indels 26; Gaps 9;

QY 6 DRRMKDHMDERAPIDPAPPSLSLKKAIKPAHCRRSAVMSVCYVQDLITLITLYTAN 65  
DB 66 BEEQTNNNGDEPDGASPPFKLSIDKKAIPKHCWKNPWTSMYSYVRDVAIVFGL-AAAA 124  
QY 66 TYIPLHPLPLVYLAWPVYWFQSCILTLGLWVLCGHHAFSEYQWIDNAVGVFLHSAALL 125  
DB 125 AYFNN-----WLVWPLYWFAQSMFWALFVLGHDGCHGFSNNHKLNSVAGHILHSSIL 178  
QY 126 TPYFSWKYSHRKHANTNSLENEEYIPRTQSOLRTYSTYFPLNTPGORILILVIMLTIG 185  
DB 179 VPYHGWIRSHRTHQNHGHVNDSEWHPLSE-----KLYNSLDDITKKFRFTLPFPLLA 232  
QY 186 PLYLLTVNSGKKYDRFTNHPDPSIPFTRERIRIOVALSDL--GIVAVFYGLKFLVQTK 242  
DB 233 YPFYLWGRSPGKK-----GSHFDPSSDLFVASEKKDVTITSTVCWTAMAALLVGLSFVM--- 285  
QY 243 GFGWVMCMYGVFVIGLNGFIIVITVYL-HHTLSS--PHYDSTENWIKGALTITDRDGLL 300

DB 286 GPLQVXLKLYGIPYWGFMVWMLDIVTLHHGHGHEKVPWYRGSEWSYLRGGLTTLDYDYGWI 345  
QY 301 NRVFHDVTHVTLHLLPPYIPIHYHAKESAIAKILGDY 339  
DB 346 NNIHHDI-GTHVIHLLFPQIPHYHLVEATEAKPVLGKY 383

RESULT 15  
T15039  
omega-3 fatty acid desaturase (EC 1.14.99.-), chloroplast - parsley  
C/Species: Petroselinum crispum (parsley)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: T15039  
R/Kirsch, C.; Takamiya-Wik, M.; Reinold, S.; Hahlbrock, K.; Somssich, I.E.  
Proc. Natl. Acad. Sci. U.S.A. 94, 2079-2084, 1997  
A/Title: Rapid, transient, and highly localized induction of plastidial omega-3 fatty aci  
A/Reference number: Z18273; MUID:97203190; PMID:9050908  
A/Accession: T15039  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: mRNA  
A/Residues: 1-438 <KIR>  
A/Cross-references: UNIPROT:P93452; UNIPARC:UPI00000A57CA; EMBL:U75745; NID:G1786065; PII  
C/Genetics:  
A/Genome: nuclear  
C/Function:  
A/Pathway: fatty acid biosynthesis  
A/Note: involved in pathogen defense response  
C/Superfamily: fatty acid (acyl-CoA) desaturase  
C/Keywords: chloroplast; oxidoreductase

Query Match 29.4%; Score 612.5; DB 2; Length 438;  
Best Local Similarity 35.1%; Pred. No. 8.2e-44;  
Matches 129; Conservative 70; Mismatches 133; Indels 35; Gaps 11;

QY 14 MDERAPIDPA---PFSLSDLKKAIPAHCRRSAVMSVCYVQDLITLITLYTANTYIPH 70  
DB 78 VEENEEDPDGAAPPFKLSIDVRAAIPKHCWVKDPVRSMSYVLRDLVIVFGL-AVAASPVNN 136  
QY 71 LPPPLVYLAWPVYWFQSCILTLGLWVLCGHHAFSEYQWIDNAVGVFLHSAALLTPYPS 130  
DB 137 -----WAVWPLYWIAQGMFWALFVLGHDGCHGFSNDAKLNSVGVHILHSSILVYPYHG 190  
QY 131 WKYSHRKHANTNSLENEEYIPRTQSOLRTYSTYFPLNTPGORILILVIMLTGLFPPLYL 190  
DB 191 WRISHRTHQNHGHVNDSEWHPLSE-----KLFNSLDDLTTRKFRFTLPFPLMAYPFYL 244  
QY 191 LTNVSGKKYDRFTNHPDPSIPFTRERIRIOVALSDL--GIVAVFYGLKFLVQTKGFGW 247  
DB 245 WGRSPGKK---GSHYDPSSDLFVPNERKDVITSTVCWTAMAALLVGLNFVM--GPVKM 297  
QY 248 MCMYGVVIGLNSFIIVTYLHHTLSS--PHYDSTENWIKGALTITDRDGLLNRPVH 305  
DB 298 LMLYGIPIYWIWVWMLDFVTVLHHGHDDKLPWYRGKESYLRGGLTTLDYDYGWNNIHH 357  
QY 306 DVTHVTLHLLFPYIPIHYHAKESAIAKILGDY----RMIDRTPF--FKAMWREAKECI 359  
DB 358 DI-GTHVVVHLLFPQIPHYHLVEATEAKPVLGKYREPKSGPVPFHLATLWKSFKKH 416  
QY 360 YIEQDAD 366  
DB 417 FVSDTGD 423

Search completed: September 22, 2006, 19:44:07  
Job time : 43 secs

GenCore version 5.1.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:35:06 ; Search time 300 Seconds  
(without alignments)  
1165.520 Million cell updates/sec

Title: US-10-622-774-2  
Perfect score: 2086  
Sequence: 1 MSDSYDDRMKDHMDERAPI.....IYIEQDADSKHGTYWYHKM 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID             | Description        |
|------------|--------|-------------|--------|----------------|--------------------|
| 1          | 2086   | 100.0       | 378    | 2 Q6S9E1_STOLA | Q6S9e1 stokesia la |
| 2          | 1537.5 | 73.7        | 377    | 2 Q7XA13_HELAN | Q7xa13 helianthus  |
| 3          | 1523.5 | 73.0        | 377    | 2 Q9SCG2_CALOF | Q9scg2 calendula o |
| 4          | 1493   | 71.6        | 374    | 2 Q65771_CREPI | Q65771 crepis pala |
| 5          | 1424.5 | 68.3        | 375    | 1 FAD12_CREAL  | Q81931 crepis alpi |
| 6          | 1410   | 67.6        | 326    | 2 Q7XA09_9ASTR | Q7xa09 dimorphothe |
| 7          | 1369   | 65.6        | 326    | 2 Q7XA08_9ASTR | Q7xa08 helichrysus |
| 8          | 1351   | 64.8        | 326    | 2 Q7XA10_RUDHI | Q7xa10 rudbeckia h |
| 9          | 1290.5 | 61.9        | 383    | 2 Q9SP28_VERGA | Q9sp28 vernonia ga |
| 10         | 1284.5 | 61.6        | 383    | 2 Q9SP29_VERGA | Q9sp29 vernonia ga |
| 11         | 1279   | 61.3        | 383    | 2 Q82729_EOROF | Q82729 borago offi |
| 12         | 1274   | 61.1        | 383    | 2 Q6DMQ8_TOBAC | Q6dmq8 nicotiana t |
| 13         | 1274   | 61.1        | 383    | 2 Q2VG85_9ROSI | Q2vg85 jatropha co |
| 14         | 1271   | 60.9        | 383    | 2 Q41305_SOLCO | Q41305 solanum cu  |
| 15         | 1268.5 | 60.8        | 379    | 2 Q65772_9ASTR | Q65772 crepis pala |
| 16         | 1265   | 60.6        | 387    | 2 Q84UB7_PUNGR | Q84ub7 punica gran |
| 17         | 1264   | 60.6        | 383    | 2 Q8G2C3_VERFO | Q8g2c3 vernicia fo |
| 18         | 1261   | 60.5        | 383    | 2 Q5S3X7_TROMA | Q5s3x7 tropaeolum  |
| 19         | 1260   | 60.4        | 382    | 2 Q8H943_SPIOL | Q8h943 spinacia ol |
| 20         | 1260   | 60.4        | 383    | 2 Q461Q1_HEVEA | Q461q1 hevea bras  |
| 21         | 1260   | 60.4        | 383    | 2 Q4QWZ0_OLEEU | Q4qwz0 olea europa |
| 22         | 1258   | 60.3        | 383    | 2 Q9LL77_SESIN | Q9lll7 sesamum ind |
| 23         | 1255.5 | 60.2        | 382    | 2 Q8W2E9_HELAN | Q8w2e9 helianthus  |
| 24         | 1255   | 60.2        | 387    | 2 Q84VT2_PUNGR | Q84vt2 punica gran |
| 25         | 1252.5 | 60.0        | 382    | 2 Q8H2C3_PERAE | Q8h2c3 persea amer |
| 26         | 1250   | 59.9        | 383    | 2 Q5FP99_SOYBN | Q5fp99 glycine max |
| 27         | 1250   | 59.9        | 383    | 2 Q6QJM6_CUCPE | Q6qjm6 cucurbita p |
| 28         | 1242.5 | 59.6        | 383    | 2 Q9AT72_CALOF | Q9at72 calendula o |
| 29         | 1240   | 59.4        | 378    | 2 Q38JF7_LINUS | Q38jf7 linum usita |
| 30         | 1240   | 59.4        | 382    | 2 Q24471_PETCR | Q24471 petroselinu |
| 31         | 1239   | 59.4        | 383    | 2 Q8W2F0_HELAN | Q8w2f0 helianthus  |

|    |        |      |     |                |                    |
|----|--------|------|-----|----------------|--------------------|
| 32 | 1238   | 59.3 | 383 | 2 Q8GVC9_OLEEU | Q8gvc9 olea europa |
| 33 | 1234   | 59.2 | 383 | 1 FDGE2_SOYBN  | P48631 glycine max |
| 34 | 1230.5 | 59.0 | 346 | 2 O81364_PRUAR | O81364 prunus arme |
| 35 | 1226   | 58.8 | 383 | 2 O23956_GOSHI | O23956 gossypium h |
| 36 | 1219.5 | 58.5 | 384 | 2 Q8W2B9_GOSHI | Q8w2b9 gossypium h |
| 37 | 1216.5 | 58.3 | 384 | 2 Q9ZP12_9BRAS | Q9zp12 brassica ca |
| 38 | 1216   | 58.3 | 379 | 2 Q4FNJ0_ARAHY | Q4fnj0 arachis hyp |
| 39 | 1216   | 58.3 | 379 | 2 Q9LKK5_9FABA | Q9llk5 arachis dur |
| 40 | 1215   | 58.2 | 383 | 1 FAD6E_ARATH  | P46313 arabidopsis |
| 41 | 1214.5 | 58.2 | 385 | 2 O23955_GOSHI | O23955 gossypium h |
| 42 | 1214   | 58.2 | 379 | 2 O22628_ARAHY | O22628 arachis hyp |
| 43 | 1210.5 | 58.0 | 384 | 2 O8LPE8_BRACM | O8lpe8 brassica ca |
| 44 | 1210   | 58.0 | 379 | 2 Q4UL26_ARAHY | Q4ul26 arachis hyp |
| 45 | 1209   | 58.0 | 384 | 2 Q9FV88_PETCR | Q9fv88 petroselinu |

ALIGNMENTS

RESULT 1  
Q6S9E1 STOLA PRELIMINARY; PRT; 378 AA.  
AC Q6S9E1.  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE Delta 12 fatty acid epoxigenase.  
OS Stokesia laevis (Stokes' aster).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
OC Vernoniaeae; Stokesia.  
OX NCBI\_TaxID=13696;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RA Hatanaka T., Hildebrand D.F.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC EMBL; AY462108; AAR23815.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
DR InterPro; IPR012261; FA\_acyl-CoA\_des.  
DR InterPro; IPR005804; FA\_desat.  
DR InterPro; IPR010257; FA\_desat\_sub.  
DR Pfam; PF00487; FA\_desaturase; 1.  
DR PIRSF; PIRSF000347; FA\_acyl-CoA\_des; 1.  
DR ProDom; PD001081; FA\_desat\_sub; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 378 AA; 44164 MW; 4DE2346FDB19BE3A CRC64;

Query Match 100.0%; Score 2086; DB 2; Length 378;  
Best Local Similarity 100.0%; Pred. No. 2e-167;  
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |                                |   |  |     |
|----|-----|--------------------------------|---|--|-----|
| QY | 1   | MSDSYDDRMKDHMDERAPI            | D | PAPPSLSDLKKAIPAHCFRRSAVSSCYVQDLITFLL           | 60  |
| DB | 1   | MSDSYDDRMKDHMDERAPI            | D | PAPPSLSDLKKAIPAHCFRRSAVSSCYVQDLITFLL           | 60  |
| QY | 61  | YTVANTYI                       | P | HLPPPLVYLAWPVVFCQSCILGLWLHGCHGHAFSEQWIDNAVGFVL | 120 |
| DB | 61  | YTVANTYI                       | P | HLPPPLVYLAWPVVFCQSCILGLWLHGCHGHAFSEQWIDNAVGFVL | 120 |
| QY | 121 | HSALITPYFSWKYSHRKHANTNSLENEEVI | P | RTOSQLRTYSTYFELDNTPGRIILVI                     | 180 |
| DB | 121 | HSALITPYFSWKYSHRKHANTNSLENEEVI | P | RTOSQLRTYSTYFELDNTPGRIILVI                     | 180 |
| QY | 181 | MLTGLPPLYLLTNVSKKYDRFTNHPD     | L | SPITTEIRIOVALSDLGIVAVFGLFLVQ                   | 240 |

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Db 181 MLTGFPYLLTNVSGKKYDRFTNHPDLPSPFTFRERIQVWISDILGILAVLVATKLLVEAKG 240
Qy 241 TKGFGWNCMYGVPVIGLNSFIIVITLHHTHLSPPHYDSTENWIKGALTITDRDFGLL 300
Db 241 TKGFGWNCMYGVPVIGLNSFIIVITLHHTHLSPPHYDSTENWIKGALTITDRDFGLL 300
Qy 301 NRVPDVTHTVHLHLPYIPHYHAKESAEIKPILGDYRMIDRTPFPKAMWREAKECIIY 360
Db 301 NRVPDVTHTVHLHLPYIPHYHAKESAEIKPILGDYRMIDRTPFPKAMWREAKECIIY 360
Qy 361 IEQDADSKHGTYWYHKM 378
Db 361 IEQDADSKHGTYWYHKM 378

RESULT 2
ID Q7XAL3_HELAN PRELIMINARY; PRT; 377 AA.
AC Q7XAL3_
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Delta12-fatty acid acetylase.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22674157; PubMed=12787248;
RX DOI=10.1046/j.1365-3113X.2003.01757.x;
RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
RT "Fungal responsive fatty acid acetylases occur widely in
RT evolutionarily distant plant families.";
RL Plant J. 34:671-683(2003).

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CC
CC
DR EMBL; AY166773; AAC38032.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006636; P:fatty acid desaturation; IEA.
DR InterPro; IPR012261; P:acyl-CoA_des.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
KW Oxidoreductase.
FT NON TER 377
SQ SEQUENCE 377 AA; 43751 MW; 832C8A129C6C2A55 CRC64;

Query Match 73.7%; Score 1537.5; DB 2; Length 377;
Best Local Similarity 72.8%; Pred. No. 46-121;
Matches 273; Conservative 41; Mismatches 54; Indels 7; Gaps 3;

Qy 8 RMKD-----HMDERAPIDPAPFSLDLKKAIPAHCFRISAVWSSCYVVDLIITFLYTV 63
Db 6 RMSDSESGKNILIERVPIDP-PFTLSDLKKAIPAHCFERSVIRSSYVVHDLIVAVFYPL 64

64 ANTYIPLPPPLVYLAWPYWYFQCSCILTGLVWLGHECGHAFSEYQWIDNAGFVLHSA 123
Db 65 ANTYIPLPTWAYLAWPYWYFQCASILTGLVWLGHECGHAFSDYQLDIDIVGFVLHSA 124

124 LPTPFSWKYSHRKHANTNSLENEEVIYIPRTQSOLRTYSTVEFLDNTPGRTILILVIMLT 183
Db 125 LPTPFSWKYSHRNHANTNSLDNEVYIPKRAKAVVYS--KLLNNPGRVFTLVFRLT 182

184 LGFPYLLTNVSGKKYDRFTNHPDLPSPFTFRERIQVWISDILGILAVLVATKLLVEAKG 243
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Db 183 LGFPYLLTNVSGKKYGRFANHPDLPSPFTFRERIQVWISDILGILAVLVATKLLVEAKG 242
Qy 244 FGWNCMYGVPVIGLNSFIIVITLHHTHLSPPHYDSTENWIKGALTITDRDFGLLNRV 303
Db 243 AAWTCMYLIPVLGVHMFVLLITLHHTHLSPPHYDSTENWIKGALTITDRDFGLNVR 302
Qy 304 PHDVHTHTVHLHLPYIPHYHAKESAEIKPILGDYRMIDRTPFPKAMWREAKECIIYEQ 363
Db 303 PHDVHTHTVHLHLSYIPHYHAKESAEIKPVLGEPFYKIDRTPFKAMWREAKECIIYEP 362
Qy 364 DADSKHGTYWYHKM 378
Db 363 DEDSEHGTYWYHKM 377

RESULT 3
ID Q9SCG2_CALOF PRELIMINARY; PRT; 377 AA.
AC Q9SCG2_
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE (8,11)-linoleoyl desaturase (Fragment).
GN Name=des8.11;
OS Calendula officinalis (Pot marigold).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Calenduleae; Calendula.
OX NCBI_TaxID=41496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=developing seed;
RX MEDLINE=20086417; PubMed=10622705; DOI=10.1016/S0014-5793(99)01541-0;
RA Fritsche K., Hornung E., Peitzsch N., Renz A., Feussner I.;
RT "Isolation and characterization of a calendic acid producing (8,11)-
RT linoleoyl desaturase.";
RL FEBS Lett. 462:249-253(1999).

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CC
CC
DR EMBL; AJ245938; CAB64256.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0006636; P:fatty acid desaturation; IEA.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
KW Oxidoreductase.
FT NON TER 377
SQ SEQUENCE 377 AA; 43615 MW; 1CBF7650955F26BF CRC64;

Query Match 73.0%; Score 1523.5; DB 2; Length 377;
Best Local Similarity 71.7%; Pred. No. 6.2e-120;
Matches 269; Conservative 45; Mismatches 54; Indels 7; Gaps 3;

Qy 8 RMKD-----HMDERAPIDPAPFSLDLKKAIPAHCFRISAVWSSCYVVDLIITFLYTV 63
Db 6 RMSDSESGKNILIERVPIDP-PFTLSDLKKAIPAHCFERSVIRSSYVVHDLIVAVFYVL 64

64 ANTYIPLPPPLVYLAWPYWYFQCSCILTGLVWLGHECGHAFSEYQWIDNAGFVLHSA 123
Db 65 ANTYIPLIPTWAYLAWPYWYFQCASILTGLVWLGHECGHAFSDYQLDIDIVGFVLHSA 124

124 LPTPFSWKYSHRKHANTNSLENEEVIYIPRTQSOLRTYSTVEFLDNTPGRTILILVIMLT 183
Db 125 LPTPFSWKYSHRNHANTNSLDNEVYIPKRAKVKIYS--KLLNNPGRVFTLVFRLT 182

184 LGFPYLLTNVSGKKYDRFTNHPDLPSPFTFRERIQVWISDILGILAVLVATKLLVEAKG 243
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Db 183 LGFPLVLLNIGSKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFAIKLLVAAG 242
QY 244 FGWVMCMYGPVIGNSFFIIVITYLHHTHLSPPHYDSTENWIKGALTITIDRDFGLLRV 303
Db 243 AAWVINWAIPLVGSVFFVLITYLHHTHLSPLPHYDSTENWIKGALTITIDRDFGLNRV 302
QY 304 FHDVTHVTHVHLFPYIPHYHAKASEAIKPIGLDYRMDTRDPFFKAMWREAKECIYIEQ 363
Db 303 FHDVTHVTHVHLHLSIYPHYHAKARDAIKPVLGEYKIDRTPIPKAMWREAKECIYIEP 362
QY 364 DADSKHKGTWYHKM 378
Db 363 DEDSEHKGVFWYHKM 377

RESULT 4
O65771_9ASTR PRELIMINARY; PRT; 374 AA.
AC O65771;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Delta 12 fatty acid epoxigenase.
OS Crepis palaestina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichorieae; Crepis.
OX NCBI_TaxID=72611;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98239771; PubMed=9572738; DOI=10.1126/science.280.5365.915;
RA Lee M., Lenman M., Banas A., Bafor M., Singh S., Schweizer M.,
RA Nilsson R., Liljenberg C., Dahlqvist A., Gummeson P.O., Sjoedahl S.,
RA Green A., Stymne S.;
RT "Identification of non-heme diiron proteins that catalyze triple bond
RT and epoxy group formation.";
RL Science 280:915-918(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lemman M.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Y16283; CAA76156.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016717; P:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006636; P:fatty acid desaturation; IEA.
DR InterPro; IPR012261; FA_acyl-CoA_des.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
DR ProDom; PD001081; FA_acyl-CoA_des; 1.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 374 AA; 43323 MW; 7764DB17BC7F426 CRC64;

Query Match 71.6%; Score 1493; DB 2; Length 374;
Best Local Similarity 70.1%; Pred. No. 2.3e-117;
Matches 260; Conservative 47; Mismatches 60; Indels 4; Gaps 2;

QY 8 RMKDHMDRAIDPAPFSLKKAIPACFRFRSAVSSCYVQDLITFLTYVNTY 67
Db 8 RTSEKSMERVSVDPTFSLSELKQAIPEPCFQSRVIRSSYYVQDLITAYIFFLANTY 67
QY 68 IPHLPPLVYLAWPVYVFCQSLTGLVWLGHCCHHAFSEYQWIDNAVGVFLHSAALLTP 127
Db 68 IPTPLTSLAYLAWPVYVFCQSVLTGLWLGHCCHHAFSNYTFWDTVGFILHSAALLTP 127
QY 128 YFSWKYSHRKHANTNSLENEEYIPRTQSLRTYSTVEFLDNTPGRIILVIMLTGLFP 187

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Db 128 YFSWKFSHRNHSNTSSIDNDVEYIPKSKSLA--RIYKLLNPPGRLLVLIIMTLGPP 185
QY 188 LYLLTNVSGKYDRFTNHFDPPLSPFTFRERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
Db 186 LYLLTNISGKYDRFANHFDPMSPIFKERERQVFLSDGLLAVFYGIKAVANKGAANV 245
QY 248 MCMYGPVIGNSFFIIVITYLHHTHLSPPHYDSTENWIKGALTITIDRDFGLLRVFDV 307
Db 246 ACMYGPVIGVTFDFVITFLHHTHQSPPHYDSTENWIRGALSATDRDFGLNSVFHDV 305
QY 308 THTHVTHVHLFPYIPHYHAKASEAIKPIGLDYRMDTRDPFFKAMWREAKECIYIEQDADS 367
Db 306 THTHVTHVHLFSYIPHYHAKARDAIKPILGDFYMDTRDTPILKAMWREGRECYIE--PDS 363
QY 368 KHKGTWYHKM 378
Db 364 KLKGVYWHKL 374

RESULT 5
FAD12_CREAL STANDARD; PRT; 375 AA.
AC O81331;
DT 24-Oct-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 2.
DT 07-FEB-2006, entry version 43.
DE Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (C-crepynate
DE synthase) (Delta-12 fatty acid acetylase).
OS Crepis alpina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichorieae; Crepis.
OX NCBI_TaxID=72610;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98239771; PubMed=9572738; DOI=10.1126/science.280.5365.915;
RA Lee M., Lenman M., Banas A., Bafor M., Singh S., Schweizer M.,
RA Nilsson R., Liljenberg C., Dahlqvist A., Gummeson P.O., Sjoedahl S.,
RA Green A., Stymne S.;
RT "Identification of non-heme diiron proteins that catalyze triple bond
RT and epoxy group formation.";
RL Science 280:915-918(1998).
CC -!- FUNCTION: Changes the delta-12 double bond of linoleic acid into a
CC triple bond in the biosynthesis of crepynic acid.
CC -!- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepynate + A +
CC H(2)O.
CC -!- COFACTOR: Iron.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- TISSUE SPECIFICITY: Seed.
CC -!- DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
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CC -----
DR EMBL; Y16285; CAA76158.2; -; mRNA.
DR InterPro; IPR012261; FA_acyl-CoA_des.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
DR Fatty acid biosynthesis; Iron; Lipid synthesis; Membrane;
KW Oxidoreductase; Transmembrane.
CHAIN 1 375
FT DELTA(12) fatty acid dehydrogenase.
FT /FTId=PRO_0000185424.
FT Potential.
FT TRANSMEM 54 74
FT TRANSMEM 77 97

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FT TRANSMEM 110 130 Potential.  
 FT TRANSMEM 172 192 Potential.  
 FT TRANSMEM 218 238 Potential.  
 FT TRANSMEM 242 262 Potential.  
 FT MOTIF 98 102 Histidine box-1.  
 FT MOTIF 134 138 Histidine box-2.  
 FT MOTIF 308 312 Histidine box-3.  
 SQ SEQUENCE 375 AA; 43382 MW; B31F5A64DD0C2926 CRC64;

Query Match 68.3%; Score 1424.5; DB 1; Length 375;  
 Best Local Similarity 65.9%; Pred. No. 1.4e-111;  
 Matches 244; Conservative 55; Mismatches 68; Indels 3; Gaps 2;

QY 8 RKQDHMDERAPIDPAPFSLDLKKAIPAHCPRRSVWSSCYVQDIIITLLTYVANTY 67  
 DB 8 RTSQKPLMERVSVD-PPTVSDLKQAIPPHCFKRSVIRSSYYVHDAIIAIVFYFLADKY 66

QY 68 IPHLPPLVYLAWPVWFCOSCIITGLVGLHCGHAFSEYQWIDNAGVFLHSALLTP 127  
 DB 67 IPILPAPLAYLAWPVWFCOSIITGLVGLHCGHAFSDYQWVDDTVGFILHSFLMTP 126

QY 128 YPSWKYSYRKHANTNSLENEVEYIPRTQSOLRTYSTYEFDLNTPGRILILVIMLTGLFP 187  
 DB 127 YPSWKYSYRHNHANTNSLNDNEVYIPKSKAKVALY--YKVLNHPGRLLIIMEITITGLFP 184

QY 188 LYLTVNSGKYDRFTNHFDPSPFITERERIQVALSDLGIVAVPYGLKFLVQTGFGQW 247  
 DB 185 LYLFTNISGKYRERFANHFDPSPFITERERQVALSDLGILAVLYGVKLAAGAAMV 244

QY 248 MCMYGVPIGLNSFIIVTYLHHTLSPPHYDSTENWIKGALTITIDRDLNRFVHDV 307  
 DB 245 TCYIGPVLGVFFPDITTYLHHTLSPPHYDSEWNWLRGALSTIDRDLNRFVHDV 304

QY 308 THTHVHLHFPYIPHYHAKESAEIKPLIGDVRMIDRTPTFFKAMWREAKECIYIQDADS 367  
 DB 305 THTHVHHLFSPYIPHYHAKESADANTVLDGPKYKIDRTPTILKAMWREAKECIPFPEKGR 364

QY 368 KHKGTYWYHK 377  
 DB 365 GSKGVYWNK 374

## RESULT 6

Q7XA09\_9ASTR PRELIMINARY; PRT; 326 AA.  
 AC Q7XA09  
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Delta12-fatty acid acetylase (Fragment).  
 OS Dimorphotheca sinuata (African daisy).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Asterids; Campanulids; Asterales; Asteraceae; Asteroidales;  
 OC Calenduleae; Dimorphotheca.  
 OC NCBI\_TaxID=112408;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22674157; PubMed=12787248;  
 RX DOI=10.1046/j.1365-3113X.2003.01757.x;  
 RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;  
 RT "Fungal responsive fatty acid acetylases occur widely in  
 evolutionarily distant plant families.";  
 RL Plant J. 34:671-683(2003).  
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 EMBL; AY166777; AAC38036.1; -; Genomic\_DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
 DR GO; GO:0006636; P:fatty acid desaturation; IEA.

DR InterPro; IPR005804; FA\_desat.  
 DR InterPro; IPR010257; FA\_desat\_sub.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR ProDom; PD001081; FA\_desat\_sub; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 FT NON\_TER 326 326  
 SQ SEQUENCE 326 AA; 9787D6D1444EA3E0 CRC64;

Query Match 67.6%; Score 1410; DB 2; Length 326;  
 Best Local Similarity 75.9%; Pred. No. 2e-110;  
 Matches 249; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

QY 31 KKAIPAHCFRRSAVWSSCYVQDIIITLLTYVANTYIPHPPLVYLAWPVWFCQSCI 90  
 DB 1 KKAIPPHCFERSLRSSYYVVDLIVAVFYFLANTYIPLLPAPLAYLAWPVWFCQASI 60

QY 91 LTGLWVLGHECGHAFSEYQWIDNAGVFLHSALLTPYFSWKYSYRKHANTNSLENEV 150  
 DB 61 LTGLWVLGHECGHAFSEYQWIDTVGFILHSALLTPYFSWKYSYRSHANTNSLNDNEV 120

QY 151 YIPRTQSOLRTYSTYEFDLNTPGRILILVIMLTGLFPYLLTNVSGKGYDRFTNHFDP 210  
 DB 121 YIPRKSQVRY--KILNPPGRVFTLVPRLTGLFPYLLTNVSGKGYRERFANHFDPMS 178

QY 211 PIFTERERIQVALSDLGIVAVPYGLKFLVQTGFGQWCMYGVPIGLNSFIIVTYLH 270  
 DB 179 PIFTERERIQVALSDLGIIAVCYALKVLVAAGATWCMYGVPIGVHAPFVLYLH 238

QY 271 THLSPPHYDSTENWIKGALTITIDRDLNRFVHDVTHTHVHLHFPYIPHYHAKESAE 330  
 DB 239 THLSLPHYDSEWNWIKGALTITIDRDLNRFVHDVTHTHVHLHLSIYIPHYHAKESAE 298

QY 331 AIKPLIGDVRMIDRTPTFFKAMWREAKEC 358  
 DB 299 AIIPVGLGEFYKIDRTPTILKAMWREAKEC 326

RESULT 7  
 Q7XA08\_9ASTR PRELIMINARY; PRT; 326 AA.  
 AC Q7XA08  
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 12.  
 DE Delta12-fatty acid acetylase (Fragment).  
 OS Helichrysum bracteatum.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Asterids; Campanulids; Asterales; Asteraceae; Asteroidales;  
 OC Gnaphalaceae; Helichrysum.  
 OC NCBI\_TaxID=220345;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22674157; PubMed=12787248;  
 RX DOI=10.1046/j.1365-3113X.2003.01757.x;  
 RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;  
 RT "Fungal responsive fatty acid acetylases occur widely in  
 evolutionarily distant plant families.";  
 RL Plant J. 34:671-683(2003).  
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 EMBL; AY166777; AAC38037.1; -; Genomic\_DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
 DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
 DR InterPro; IPR005804; FA\_desat.  
 DR InterPro; IPR010257; FA\_desat\_sub.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR ProDom; PD001081; FA\_desat\_sub; 1.

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KW Oxidoreductase.
FT NON TER 1 1
FT NON TER 326 326
SQ SEQUENCE 326 AA; 38030 MW; D355816CF4AA2829 CRC64;

Query Match 65.8%; Score 1369; DB 2; Length 326;
Best Local Similarity 73.8%; Pred. No. 5.7e-107;
Matches 242; Conservative 32; Mismatches 52; Indels 2; Gaps 1;

QY 31 KKAIPACFRSRAVSSCYVQDLITFLLYTVANTYIPIHLPPLVYLWVPVWFQSCSI 90
DB 1 KKAIPHCERSVIRSYVYXHDLYTVFYLYAXTYIIPXPAHLYLWVPVWFQASI 60

QY 91 LTGLWVLGHECGHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSHRKHANTNSLENEEV 150
DB 61 LTGLWVLGHECGHAFSDYQIDDDVGVFLHSALTPYFSWKYSHRKHANTNSLNDDEV 120

QY 151 YIPRTQSQRSTYSYFELNTPGRILILVIMLTGLGFPPLYLNTVSGKKYDRFNNHDPPLS 210
DB 121 YIPKRSKVMYIS--KILNPPGQVFTLAFRLTLGFPPLYLNTVSGKKYERFANHPDPLS 178

QY 211 PIPTERERIQVALSDIGIVAVFYGLKFLVOTKGFQWMCVMYGPVIGLNSFIIVITLHH 270
DB 179 PIPTERERIQVLSDIGIIVAVFYGLKFLVOTKGFQWMCVMYGPVIGVHAFVLLITLHH 238

QY 271 THLSPHYDSTENWIKGALTTIDRDFGLNRFVHDVTHVLHLFPYIPHYHAKESAE 330
DB 239 THLSPHYDSTENWIKGALSTIDRDFGLNRFVHDVTHVLHLHLISYIPHYHAKESAE 298

QY 331 AIKPIGLDYRMIDRTPPFKAMWREAKEC 358
DB 299 AINPVLGEYKIDRTPIFKAMWREAKEC 326

RESULT 8
Q7XA10 RUDHI PRELIMINARY; PRT; 326 AA.
AC Q7XA10;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DE Delta12-fatty acid acetylase (Fragment).
OS Rubbeckia hirta (Black-eyed Susan).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Rudbeckia.
OX NCBI_TaxID=52299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22674157; PubMed=12787248;
RX DOI=10.1046/j.1365-3113.2003.01757.x;
RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
RT "Fungal responsive fatty acid acetylases occur widely in
RT evolutionarily distant plant families.";
RL Plant J. 34:671-683(2003).
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CC -----
CC EMBL; AY166776; AAC38035.1; -; Genomic_DNA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0016491; F:oxidoreductase activity; IEA.
CC GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
CC GO; GO:0006636; P:fatty acid desaturation; IEA.
CC InterPro; IPR005804; FA_desat.
CC InterPro; IPR010257; FA_desat_sub.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD001081; FA_desat_sub; 1.
KW Oxidoreductase.
FT NON TER 1 1
FT NON TER 326 326
SQ SEQUENCE 326 AA; 37865 MW; D3C65BAD9EF25783 CRC64;

Query Match 64.8%; Score 1351; DB 2; Length 326;
Best Local Similarity 72.3%; Pred. No. 1.9e-105;
Matches 237; Conservative 37; Mismatches 52; Indels 2; Gaps 1;

QY 32 KAIPACFRSRAVSSCYVQDLITFLLYTVANTYIPIHLPPLVYLWVPVWFQSCIL 91
DB 1 KAIPHCERSVIRSYVYVHDLIVAYFYFLANTYIPLPTPWAYLWVPVWFQASIL 60

QY 92 TGLWVLGHECGHAFSEYQWIDNAVGVFLHSALLTPYFSWKYSHRKHANTNSLENEEV 151
DB 61 TGLWVLGHECGHAFSDYQIDDDVGVFLHSALTPYFSWKYSHRKHANTNSLNDDEV 120

QY 152 IPTQSQRSTYSYFELNTPGRILILVIMLTGLGFPPLYLNTVSGKKYDRFNNHDPPLSP 211
DB 121 IPKRAKAAVYS--KILNPPGQVFTLAFRLTLGFPPLYLNTVSGKKYGRFANHPDPLSP 178

QY 212 IETTERERIQVALSDIGIVAVFYGLKFLVOTKGFQWMCVMYGPVIGLNSFIIVITLHH 271
DB 179 IETTERERIQVLSDIGIIVAVFYGLKFLVOTKGFQWMCVMYGPVIGVHAFVLLITLHH 238

QY 272 HLSSPHYDSTENWIKGALTTIDRDFGLNRFVHDVTHVLHLFPYIPHYHAKESAE 331
DB 239 HLSPHYDSTENWIKGALSTIDRDFGLNRFVHDVTHVLHLHLISYIPHYHAKESAE 298

QY 332 IKPILGDYRMIDRTPPFKAMWREAKEC 359
DB 299 IKPVLGEYKIDRTPIFKAMWREAKEC 326

RESULT 9
Q9SP28 VERGA PRELIMINARY; PRT; 383 AA.
AC Q9SP28;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE Delta-12 oleate desaturase (EC 1.3.1.35).
GN Name=FAD2-2;
OS Vernonia galamensis (Ironweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Vernoniaceae; Vernonia.
OX NCBI_TaxID=83960;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=10759541;
RA Hage T.G., Seither C., Hildebrand D.;
RT "Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
RT encoding a microsomal oleate desaturase (FAD2) (accession nos.
RT AF188263 and AF188264) and functional expression in Saccharomyces
RT cerevisiae (PGR00-035).";
RL Plant Physiol. 122:1457-1457(2000).
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CC -----
CC EMBL; AF188264; AAF04094.1; -; mRNA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
CC GO; GO:0050184; P:phosphatidylcholine desaturase activity; IEA.
CC GO; GO:0006633; P:fatty acid biosynthesis; IEA.
CC GO; GO:0006636; P:fatty acid desaturation; IEA.
CC InterPro; IPR012261; FA_acyl-CoA_des.
CC InterPro; IPR005804; FA_desat.
CC InterPro; IPR010257; FA_desat_sub.
CC Pfam; PF00487; FA_desaturase; 1.
CC PIRSF; PIRSF000347; FA_acyl-CoA_des; 1.
CC ProDom; PD001081; FA_desat_sub; 1.
KW Oxidoreductase.
FT NON TER 1 1
FT NON TER 326 326
SQ SEQUENCE 383 AA; 44330 MW; 10D954DC084F7D41 CRC64;

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Query Match 61.9%; Score 1290.5; DB 2; Length 383;  
Best Local Similarity 59.2%; Pred. No. 2.9e-100;  
Matches 219; Conservative 68; Mismatches 80; Indels 3; Gaps 2;

QY 6 DDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFLTYTAN 65  
DB 13 DEKKAHEALQRPVQKPPFTVGDIKKAIPPHCFNRSVIRSFYVYDITISFIFYLAT 72  
QY 66 TYIPLPPLVYLAWPVYVFCQSCILTLGLWLGHECHHAFSEYQWIDNAGFVLHLSALL 125  
DB 73 NYIPLPPLSVAPVYVIFQGCVLTVGWVIAHECHHAFSDYQWLDOTVGLILHLSALL 132  
QY 126 TPYFSWKYSHRKHANTNSLENEEYIPRTQSLRTYSTYFELDNTPGRILILVIMLTIG 185  
DB 133 VPYFSWKYSHRHHNTSGSIEHDEVFVFKLSNVR--STARYLNNPPGRILTLVLTIG 190  
QY 186 PLYLLTNVSGKKYDRFTNHFDPISPIETERRIQVSLDGLIVAFVGLKFLVQTKGFG 245  
DB 191 WPLYLMFNVSGRYVDRFACHFDPNPSIYSNREARQIFISDAGILAVFGLFKLAMAKGLT 250  
QY 246 WYCMYGVVPVIGLNSFIIVITVYHHTLSSPHYDSTENWIKGALTTIDRPFGLLNRFVH 305  
DB 251 WYLCMYGGLLVNGFVLITLQHTPSLPHYDTTENDWLRGALATIDRDYGLLNKVFH 310  
QY 306 DVTHVHLHLFPYIPHYHAKASEAIKPILDYRMIDRTPPFKAMWREAKECIEYBODA 365  
DB 311 NITDTHVAHLFSTMPHYHAMEATKVIKPILEGYYQPDGTSIFKAMYRETKECIYVDKDE 370  
QY 366 DSKHKGTYWY 375  
DB 371 NVK-DGVYWY 379

RESULT 10  
Q9SP29\_VERGA PRELIMINARY; PRT; 383 AA.  
ID Q9SP29\_VERGA  
AC Q9SP29\_VERGA  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 24.  
DE Name=FA2D-1;  
GN Vernonia galamensis (Ironweed).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
OC Vernoniae; Vernonia.  
OX NCBI\_TaxID=83960;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=10759541;  
RA Hage T.G., Seither C., Hildebrand D.;  
RT "Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.  
RT encoding a microsomal oleate desaturase (FA2D) (accession nos.  
RT AF188263 and AF188264) and functional expression in Saccharomyces  
RT cerevisiae (PGR00-035).";  
RL Plant Physiol. 122:1457-1457(2000).  
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CC  
CC EMBL; AF188263; AAF04093.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
DR GO; GO:0050184; F:phosphatidylcholine desaturase activity; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
DR InterPro; IPR012261; FA\_acyl-CoA\_des.  
DR InterPro; IPR005804; FA\_desat.  
DR Pfam; PF00487; FA\_desaturase; 1.  
DR PIRSF; PIRSF000347; FA\_acyl-CoA\_des; 1.  
DR ProDom; PD001081; FA\_desat\_sub; 1.

Query Match 61.3%; Score 1279; DB 2; Length 383;  
Best Local Similarity 60.1%; Pred. No. 2.7e-99;

KW Oxidoreductase.  
SQ SEQUENCE 383 AA; 44268 MW; C16B93BE7F94DA80 CRC64;

Query Match 61.6%; Score 1284.5; DB 2; Length 383;  
Best Local Similarity 58.9%; Pred. No. 9.4e-100;  
Matches 218; Conservative 68; Mismatches 81; Indels 3; Gaps 2;

QY 6 DDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFLTYTAN 65  
DB 13 DEKKAHEALQRPVQKPPFTVGDIKKAIPPHCFNRSVIRSFYVYDITISFIFYLAT 72  
QY 66 TYIPLPPLVYLAWPVYVFCQSCILTLGLWLGHECHHAFSEYQWIDNAGFVLHLSALL 125  
DB 73 NYIPLPPLSVAPVYVIFQGCVLTVGWVIAHECHHAFSDYQWLDOTVGLILHLSALL 132  
QY 126 TPYFSWKYSHRKHANTNSLENEEYIPRTQSLRTYSTYFELDNTPGRILILVIMLTIG 185  
DB 133 VPYFSWKYSHRHHNTSGSIEHDEVFVFKLSNVR--STARYLNNPPGRILTLVLTIG 190  
QY 186 PLYLLTNVSGKKYDRFTNHFDPISPIETERRIQVSLDGLIVAFVGLKFLVQTKGFG 245  
DB 191 WPLYLMFNVSGRYVDRFACHFDPNPSIYSNREARQIFISDAGILAVFGLFKLAMAKGLT 250  
QY 246 WYCMYGVVPVIGLNSFIIVITVYHHTLSSPHYDSTENWIKGALTTIDRPFGLLNRFVH 305  
DB 251 WYLCMYGGLLVNGFVLITLQHTPSLPHYDTTENDWLRGALATIDRDYGLLNKVFH 310  
QY 306 DVTHVHLHLFPYIPHYHAKASEAIKPILDYRMIDRTPPFKAMWREAKECIEYBODA 365  
DB 311 NITDTHVAHLFSTMPHYHAMEATKVIKPILEGYYQPDGTSIFKAMYRETKECIYVDKDE 370  
QY 366 DSKHKGTYWY 375  
DB 371 NVK-DGVYWY 379

RESULT 11  
O82729\_BOROF PRELIMINARY; PRT; 383 AA.  
ID O82729\_BOROF  
AC O82729\_BOROF  
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 26.  
DE Delta-12 fatty acid desaturase.  
OS Borago officinalis (Bourrache).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC asterids; lamiales; Boraginaceae; Borago.  
OX NCBI\_TaxID=13363;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sayanova O., Shewry P.R., Napier J.A.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC EMBL; AF074324; AAC31698.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR GO; GO:0006636; P:fatty acid desaturation; IEA.  
DR InterPro; IPR012261; FA\_acyl-CoA\_des.  
DR InterPro; IPR005804; FA\_desat.  
DR Pfam; PF00487; FA\_desaturase; 1.  
DR PIRSF; PIRSF000347; FA\_acyl-CoA\_des; 1.  
DR ProDom; PD001081; FA\_desat\_sub; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 383 AA; 44048 MW; 13DF2BD876E7E5EF CRC64;

Query Match 61.3%; Score 1279; DB 2; Length 383;  
Best Local Similarity 60.1%; Pred. No. 2.7e-99;

| Matches | 218; | Conservative   | 62; | Mismatches | 81; | Indels | 2; | Gaps | 17; |
|---------|------|--|-----|------------|-----|--------|----|------|-----|
| Qy      | 13   | DMDERAPIDPAPFSLSDLKKAIPACFCRRSAWVSCYYVQDLITITFLTYVTANTYIPIHLP  | 72  |            |     |        |    |      |     |
| Db      | 19   | DVFQRPSEKPPFTVGDLKKVIPPHCFORSVLHSFSYVYDLVIAALFFYTSASRYHLQP     | 78  |            |     |        |    |      |     |
| Qy      | 73   | PPLVYLAWPVYWCOSCLITGLWLHGCHHASEYQWIDNACFVLHSAALLTPYESWK        | 132 |            |     |        |    |      |     |
| Db      | 79   | HPLSYAWPLWYFCQGSVLTVGVWIAHECGHAFSDYQWLDDTVGLLHLSALLVPYFSWK     | 138 |            |     |        |    |      |     |
| Qy      | 133  | YSHRKHANTNSLENEEYVIPRTOSQLRTSYTFEFLDNTPGRIILIVMLTGLGPPLYLLT    | 192 |            |     |        |    |      |     |
| Db      | 139  | YSHRRHSNTGSLERDEVFVFKRSGISWSS--EVLNPPGRLVLVLLVQLTLGWPLYLMP     | 196 |            |     |        |    |      |     |
| Qy      | 193  | NVSGKKYDRPTNHPDPDSPITEBERIQVALSDGIVAVFGLGKFLVOTKGFGWVMCMYG     | 252 |            |     |        |    |      |     |
| Db      | 197  | NVSGRPYDFRACHFDPKSPINYNDERLQIYISDAGIVAVMYGLYRLVAAKGVAWVCVYG    | 256 |            |     |        |    |      |     |
| Qy      | 253  | VPVIGLANSFIIVTYLHHHTLSSPHYDSTENWTKGALTITTDROFGLLNRYFDVDTHTHV   | 312 |            |     |        |    |      |     |
| Db      | 257  | VPLLVVNGFLVLIYLOHTQPSLPHYDSSEMDLKGALATVDROYGFLNKVLHMTDTHV      | 316 |            |     |        |    |      |     |
| Qy      | 313  | LHLHLPYIPHYHAKEASEAIKPIILDGYRMDITPTFPFKAMWREAKECIYIEODADSKHGKT | 372 |            |     |        |    |      |     |
| Db      | 317  | AHHLFSTMPHYHAMEATKAIKPILDGYQCORTPVFKAMYREVKECIYVEADEGNNKGV     | 376 |            |     |        |    |      |     |
| Qy      | 373  | WYV 375  |     |            |     |        |    |      |     |
| Db      | 377  | FWY 379  |     |            |     |        |    |      |     |

```

RESULT 12
Q6DMQ8_TOBAC PRELIMINARY; PRT; 383 AA.
ID Q6DMQ8_TOBAC
Q6DMQ8;
AC AC
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 2.
DT 07-FEB-2006, entry version 13.
DE Microsomal omega-6-desaturase.
GN Name=FAD2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wisconsin 38;
RA Yang M., Zheng G., Zhang F., Xu Y.;
RT "FAD2-silencing has pleiotropic effect on polar lipids of leaves and
RL varied effect in different organs of transgenic tobacco.";
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wisconsin 38;
RA Yang M.F., Zhang F.Y., Zheng G.L., Xu Y.N.;;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.
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CC -----
CC EMBL; AY650024; AAT72296.2; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006636; P:fatty acid desaturation; IEA.
DR InterPro; IPR012361; FA_acyl-CoA_des.
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRISF; PRISF000347; FA_acyl-CoA_des; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
DR Oxidoreductase.
KW

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|        |  |   |  |
|--------|--|---|--|
| 5Q     | SEQUENCE   | 383 AA; 43933 MW; 7D75199984305393 CRC64;                           |  |
|        | Query Match  | 61.1%; Score 1274; DB 2; Length 383;                                |  |
|        | Best Local Similarity  | 58.6%; Pred. No. 7.2e-99;   |  |
|        | Matches  | 211; Conservative 67; Mismatches 80; Indels 2; Gaps 1;              |  |
| QY     | 16   | ERAPIDAPFSLDKKAIPAHCFRRASVSSCVVODLITFLFYLTVANTYIPIHLPPPL 75         |  |
| DB     | 22   | EKVPTSPKPPVTGDIKKAIPHCPCQSLVRSFSVYVDLILVSYFYIATYIFHLLSPY 81         |  |
| QY     | 76   | VYLAWPYVFCQSCILTGLWLGHECGHAFSEYQWIDNAGVFLHSAITPPYFSWKYSH 135        |  |
| DB     | 82   | CYLAWPIYWCQCVCTGIWVIAHECGHAFSDYQWVDDTVGLILHSALAMVPYFSWKYSH 141      |  |
| QY     | 136  | RKHANTNSLENEBVIYIPRTQSQRITSTVTEFLDNTFCRILILVIMLTIGFPLYLLTNVS 195    |  |
| DB     | 142  | RRHSNTGSLERDEVFVKPKSLQMGYSKY--LNNPFCRVMSLTAVTTLTGLMPLYLAFNVS 199    |  |
| QY     | 196  | GKXYDRFTNHFDPPLSPFTFRERIQVALSDLGIIVAFVGLKFLVQTKGFGVMCMYGVDP 255     |  |
| DB     | 200  | GRHYDRFACHYDPVGPILYNDREURQIFLSDAGVAGAGYLLVRIALVKGIAELVCMYGPL 259    |  |
| QY     | 256  | IGLNSFTIIVITYLHHTLHSLSPHYDSTENWMIKGLATTIDRDFGLLNRVFDHVTHTVLHH 315   |  |
| DB     | 260  | LIVNGFLVLITYLQHTHPSLPHYDSSEWMLRGALATVDRDYGILNKVFHNITDTHVVHH 319     |  |
| QY     | 316  | LPFYIPHYHAKASEAIKPILGDRYMDTRTFFKAMMREAKECIYIISODADSKHGKGTWY 375     |  |
| DB     | 320  | LFTSMTPHYNAMEATKAVKPLLLGDDYQFDGTPVFKAMMREAKECIYVBEKDEASQCKGVFWY 379 |  |
| RESULT | 13   |   |  |
| ID     | Q2VG85_9PROSI  | PRELIMINARY; PRT; 383 AA.   |  |
| AC     | Q2VG85;  |   |  |
| DT     | 10-JAN-2006,   | integrated into UniProtKB/TREMBL.                                   |  |
| DT     | 10-JAN-2006,   | sequence version 1.   |  |
| DT     | 07-MAR-2006,   | entry version 4.  |  |
| DE     | Delta12-fatty acid   | desaturase.   |  |
| OS     | Jatropha curcas.   |   |  |
| OC     | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |   |  |
| OC     | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;   |   |  |
| OC     | rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;   |   |  |
| OC     | Jatrophaeae; Jatropha.   |   |  |
| OX     | NCBI_TaxID=180498;   |   |  |
| ON     | NCBI_TaxID=180498;   |   |  |
| RP     | NUCLEOTIDE SEQUENCE.   |   |  |
| RA     | Qing R., Guo L., Luo T., Xu Y., Tang L., Li H., Chen P.;   |   |  |
| RT     | "Identification and characterization of a novel delta12-fatty acid   |   |  |
| RT     | desaturase gene from higher plant Jatropha curcas."  |   |  |
| RL     | Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.  |   |  |
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| CC     | Distributed under the Creative Commons Attribution-NoDerivs License  |   |  |
| CC     | -----  |   |  |
| CC     | EMBL; DQ157776; ABA41034.1; -; mRNA.   |   |  |
| DR     | Oxidoreductase.  |   |  |
| KW     | SEQUENCE 383 AA; 44473 MW; 8ACD0F2444017D92 CRC64;   |   |  |
| SO     | SEQUENCE   |   |  |

|    | Query Match           | 61.1%            | Score 1274;        | DB 2;              | Length 383;        |
|----|-----------------------|------------------|--------------------|--------------------|--------------------|
|    | Best Local Similarity | 59.2%;           | Pred. No. 7.2e-99; |                    |                    |
|    | Matches 213;          | Conservative 63; | Mismatches 82;     | Indels 2;          | Gaps 1;            |
| Qy | 16                    | ERAPIDAPFSLDKKAI | PAHCFRRSAGVSSC     | VQDLIITFLLYTVANTYI | PHLPPL 75          |
| Db | 22                    | KRPYSKPPTLGQVKAI | PPHCFQSRSLRSFS     | VVYDYLTAIFYVATNY   | FHLLPQL 81         |
| Qy | 76                    | VYLAWPVYFCQSCIL  | TGLVWLHGECGHAF     | SEYQWIDNAVGVFLH    | SALLTPYFSWKYSH 135 |
| Db | 82                    | SYVAMPYWSLGGCV   | LGTGIWVIAHECGHAF   | SDYQWLDLIDVGLLLH   | SCLLVPYFSWKHSH 141 |
| Qy | 136                   | RKHANTNSLENEBVI  | YPRQSQRLTYSTVTE    | FLDNTFCRILILVIML   | TGFPYLLTNVS 195    |



|    |     |        |        |        |        |       |      |      |      |      |     |      |      |      |
|----|-----|--------|--------|--------|--------|-------|------|------|------|------|-----|------|------|------|
| Db | 244 | LGWVLA | MYGGLV | VNGFLV | LITFLQ | THASL | PHYD | STEN | WLRG | ALAT | IDR | DYGI | LNKV | 303  |
| Qy | 304 | FHDV   | THVL   | HLPY   | I      | PHYH  | AK   | SEAT | KPIL | G    | YR  | MD   | TRT  | PPFK |
| Db | 304 | FHNIT  | DTHV   | THHL   | FST    | MPHY  | HAME | ATK  | KPIL | G    | YR  | MD   | TRT  | PPFK |
| Qy | 364 | DADSK  | HKG    | TYWY   | 375    |       |      |      |      |      |     |      |      |      |
| Db | 364 | DAEVK  | -DGV   | WY     | 374    |       |      |      |      |      |     |      |      |      |

Search completed: September 22, 2006, 19:43:23  
Job time : 304 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2006, 23:03:22 ; Search time 7201 Seconds  
(without alignments)  
10918.286 Million cell updates/sec

Title: US-10-622-774-1  
Perfect score: 1406  
Sequence: 1 gtaggtttgggtcggtg.....aaaaaaaaaaaaaaaaaaaaa 1406

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 564.6 | 40.2        | 1047   | 10    | DW097268    |
| 2          | 509.8 | 36.3        | 982    | 10    | DW097410    |
| 3          | 503.2 | 35.8        | 941    | 10    | DW158633    |
| 4          | 495.4 | 35.2        | 937    | 10    | DW085008    |
| 5          | 493.2 | 35.1        | 921    | 10    | DW093963    |
| 6          | 493.2 | 35.1        | 922    | 10    | DW094502    |
| 7          | 493.2 | 35.1        | 927    | 10    | DW097606    |
| 8          | 492.2 | 35.0        | 922    | 10    | DW094732    |
| 9          | 491.8 | 35.0        | 906    | 10    | DW093673    |
| 10         | 491.6 | 35.0        | 928    | 10    | DW089055    |
| 11         | 485.2 | 34.5        | 898    | 10    | DW090169    |
| 12         | 483.4 | 34.4        | 893    | 10    | DW089237    |
| 13         | 483   | 34.4        | 942    | 10    | DW097931    |
| 14         | 481.2 | 34.2        | 919    | 10    | DW089183    |
| 15         | 480.8 | 34.2        | 908    | 10    | DW096275    |
| 16         | 479.4 | 34.1        | 885    | 10    | DW128132    |
| 17         | 479   | 34.1        | 906    | 10    | DW090949    |
| 18         | 475.8 | 33.8        | 906    | 10    | DW097416    |
| 19         | 475.4 | 33.8        | 953    | 10    | DW097829    |

|    |       |      |     |    |          |
|----|-------|------|-----|----|----------|
| 20 | 474.4 | 33.7 | 878 | 10 | DW084498 |
| 21 | 471.8 | 33.6 | 906 | 10 | DW098114 |
| 22 | 470.4 | 33.5 | 863 | 10 | DW114098 |
| 23 | 469.4 | 33.4 | 907 | 10 | DW093425 |
| 24 | 465   | 33.1 | 866 | 10 | DW084816 |
| 25 | 464.8 | 33.1 | 902 | 10 | DW094062 |
| 26 | 464.2 | 33.0 | 964 | 10 | DW119170 |
| 27 | 464   | 33.0 | 866 | 10 | DW084758 |
| 28 | 464   | 33.0 | 871 | 10 | DW079511 |
| 29 | 461   | 32.8 | 886 | 10 | DW092156 |
| 30 | 459.8 | 32.7 | 897 | 10 | DW094175 |
| 31 | 455   | 32.4 | 897 | 10 | DW091892 |
| 32 | 454.6 | 32.3 | 879 | 10 | DW097724 |
| 33 | 448   | 31.9 | 906 | 10 | DW097104 |
| 34 | 446   | 31.7 | 849 | 10 | DW094401 |
| 35 | 443.2 | 31.5 | 691 | 3  | BQ994479 |
| 36 | 440   | 31.3 | 799 | 10 | DW096751 |
| 37 | 437.2 | 31.1 | 685 | 10 | DT211274 |
| 38 | 436.2 | 31.0 | 862 | 10 | DW094388 |
| 39 | 434.8 | 30.9 | 849 | 10 | DW098230 |
| 40 | 433   | 30.8 | 823 | 10 | DW093011 |
| 41 | 428.6 | 30.5 | 797 | 10 | DW087447 |
| 42 | 423.4 | 30.1 | 798 | 10 | DW048664 |
| 43 | 417   | 29.7 | 859 | 10 | DW058651 |
| 44 | 416.4 | 29.6 | 844 | 10 | DW092317 |
| 45 | 415.6 | 29.6 | 785 | 10 | DW097877 |

## ALIGNMENTS

RESULT 1  
DW097268  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

DW097268 1047 bp mRNA linear EST 22-DEC-2005  
CLPX8290.bl C10.ab1 CLP(XYZ) lettuce perennis Lactuca perennis cDNA  
Clone CLPX8290, mRNA sequence.  
DW097268  
DW097268.1 GI:83895188  
EST.  
Lactuca perennis  
Lactuca perennis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.  
1 (bases 1 to 1047)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://comgenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@catc.ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.  
Location/Qualifiers  
1..1047  
/organism="Lactuca perennis"  
/mol\_type="mRNA"  
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/db\_xref="taxon:43195"  
/clone="CLPX8290"  
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/clone\_lib="CLP(XYZ) lettuce perennis"  
/note="Vector: pBRCDNASFIAB; The standard library was  
constructed from multiple sources of RNA from a single

genotype. cDNAs were then size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes (X-large, Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>

## ORIGIN

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Query Match      40.2%; Score 564.6; DB 10; Length 1047;
Best Local Similarity 75.7%; Pred. No. 1.1e-132;
Matches 728; Conservative 0; Mismatches 225; Indels 9; Gaps 2;

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DB 110 GATCGAATGAAGATCATGATATGAGCAAGAGCCCGATGATCGCGCCCATCTTCG 169
QY 95 GATCCATCTAAGGACACGATATATAAAGCGTGTCCCGTTGA---GCCACCATCTCA 151
DB 95 GATCCATCTAAGGACACGATATATAAAGCGTGTCCCGTTGA---GCCACCATCTCA 151
QY 170 TTAAGTGATCTAAAGAAAGCAATCCCTGCACATTCGTTCCGCGCATCGCGTCTGGTCA 229
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## RESULT 2

DW097410

LOCUS

DEFINITION

CLP8434\_b1.D22.ab1.CLP(XYZ) 982 bp mRNA linear EST 22-DEC-2005

Clone CLP8434, mRNA sequence.

ACCSSION

DW097410

VERSION

DW097410.1 GI:83895330

KEYWORDS

EST.

SOURCE

Lactuca perennis

ORGANISM

Lactuca perennis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.

1 (bases 1 to 982)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

<http://compenomics.ucdavis.edu/>

Unpublished (2002)

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Email: [akozik@ucdavis.edu](mailto:akozik@ucdavis.edu) [michelmore@vegmail.ucdavis.edu]

Library was sequenced at Joint Genome Institute, Walnut Creek CA,

using ABI 3730 machines.

FEATURES

Location/Qualifiers

1..982

/organism="Lactuca perennis"

/mol\_type="mRNA"

/strain="PI-274378"

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/note="Vector: pBRCNDSFAB; The standard library was

constructed from multiple sources of RNA from a single

genotype. cDNAs were then size-fractionated, directionally

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transformations made with three size classes

(X-large, Y-medium and Z-small) to minimize size bias due

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each source of RNA and library construction can be

obtained at <http://cgdb.ucdavis.edu/>

ORIGIN

Query Match

Best Local Similarity

Matches 677; Conservative 0; Mismatches 212; Indels 10; Gaps 3;

QY 110 GATCGAATGAAGATCATGATATGAGCAAGAGCCCGATGATCGCGCCCATCTTCG 169

DB 94 GATCCATCTAAGGACACGATATATAAAGCGTGTCCCGTTGA---GCCACCATCTCA 150

QY 170 TTAAGTGATCTAAAGAAAGCAATCCCTGCACATTCCTTCGCGCATCGCGTCTGGTCA 229

DB 151 CTAAGTGATCTCAAGAAAGCAATCCCTGCCATTCCTTCGAGCGCTCACTCATCGTTCA 210

QY 230 TCCTGCTACGAGTGTTCAGGATCTCATATCATCTTCTCTTTTATATACACGCGTCCCAACACC 289





SOURCE Lactuca perennis  
ORGANISM Lactuca perennis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
1 (bases 1 to 921)  
Lin.H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J.,  
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,  
Lai,Z., Church,S., Jackson,L. and Bradford,K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compgenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmoe]  
Department of Vegetable Crops, R.W.Michelmoe Lab  
University of California at Davis (UCD)  
Amsundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akosik@ucdavis.org [michelmoe@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
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FEATURES  
source Location/Qualifiers  
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cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at http://cgpdb.ucdavis.edu/"

Query Match 35.1%; Score 493.2; DB 10; Length 921;  
Best Local Similarity 76.0%; Pred. No. 1.8e-114;  
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ACCESSION CLPY5660 bi G24.ab1 CLP(XYZ) lettuce perennis Lactuca perennis cDNA  
VERSION DW094502.1 GI:83892422  
KEYWORDS EST.  
SOURCE Lactuca perennis  
ORGANISM Lactuca perennis  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorioideae; Lactuca.  
1 (bases 1 to 922)  
Kozik,A., Michelmoe,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
Lin.H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J.,  
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,  
Lai,Z., Church,S., Jackson,L. and Bradford,K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compgenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmoe]  
Department of Vegetable Crops, R.W.Michelmoe Lab  
University of California at Davis (UCD)  
Amsundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
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Email: akosik@ucdavis.org [michelmoe@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.  
FEATURES  
source Location/Qualifiers  
1..922  
/organism="Lactuca perennis"  
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constructed from multiple sources of RNA from a single

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## ORIGIN

Query Match 35.1%; Score 493.2; DB 10; Length 922;  
Best Local Similarity 76.0%; Pred. No. 1.8e-114;  
Matches 638; Conservative 0; Mismatches 193; Indels 9; Gaps 2;

QY 110 GATCGAATGAAGATCATGATATGACGACGAGCCCGATGATCGCGCCATCTTCG 169  
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LOCUS

DW097606 927 bp mRNA linear EST 22-DEC-2005

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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clone CLPY8633, mRNA sequence.  
DW097606.  
DW097606.1 GI:83895526  
EST.  
Lactuca perennis  
Lactuca perennis

REFERENCE  
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.  
1 (bases 1 to 927)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compgenomics.ucdavis.edu/>  
Unpublished (2002)

## TITLE

JOURNAL  
COMMENT

Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.

FEATURES  
source

1..927  
Location/Qualifiers  
/organism="Lactuca perennis"  
/mol\_type="mRNA"  
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genotype. cDNAs were then size-fractionated, directionally  
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transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
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each source of RNA and library construction can be  
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Query Match 35.1%; Score 493.2; DB 10; Length 927;  
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Matches 638; Conservative 0; Mismatches 193; Indels 9; Gaps 2;

QY 110 GATCGAATGAAGATCATGATATGACGACGAGCCCGATGATCGCGCCATCTTCG 169  
DB 97 GATCCATCTAAGGACACGATATATAAAGCGTGCCCGGTGA---GCCACCATTC 153  
QY 170 TTAAGTGATCTAAGAAAGCAATCCCTGCACATTCCTCCGCGATCGCGCTCGGTCA 229  
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DB 334 CAAGCTAGCATTTCTTACTGGCTTATGGGTCAATCGGTGATGATGTTGTCACCATGCCCTT 393  
QY 410 AGTGAGTACCAAGTGAATGATAACCGCGTGTGATTCGTCTCCTCCTCAATTCGGCTCTCCTCACC 469





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RESULT 9
DW093673
LOCUS
DEFINITION
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  CLP4893.b1.124.ab1 CLP(XYZ) lettuce perenniss Lactuca perenniss cDNA
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ACCESSION
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VERSION
  EST.
KEYWORDS
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  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
  Cichorieae; Lactuca.
  1 (bases 1 to 906)
REFERENCE
  AUTHORS
    Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
    Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
    Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
    Lai,Z., Church,S., Jackson,L. and Bradford,K.
  TITLE
    Lettuce and Sunflower ESTs from the Compositae Genome Project
  JOURNAL
    http://compgenomics.ucdavis.edu/
  COMMENT
    Unpublished (2002)
    Contact: Alexander Kozik [R.W.Michelmore]
    Department of Vegetable Crops, R.W.Michelmore Lab
    University of California at Davis (UCD)
    Asmundson Hall, UCD, Davis, CA 95616, USA
    Tel: 1-(530)-742-1742
    Fax: 1-(530)-752-9659
    Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
    Library was sequenced at Joint Genome Institute, Walnut Creek CA,
    using ABI 3730 machines.
FEATURES
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    constructed from multiple sources of RNA from a single
    genotype. cDNAs were then size-fractionated, directionally
    cloned into a custom medium-copy vector and
    transformations made with three size classes
    (X-large, Y-medium and Z-small) to minimize size bias due
    to differential transformation efficiency. Details of
    each source of RNA and library construction can be
    obtained at http://cgpdb.ucdavis.edu/"
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  Query Match 35.0%; Score 491.8; DB 10; Length 906;
  Best Local Similarity 75.7%; Pred. No. 4.2e-114;
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    DW089055.1 GI:83886975
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    Lactuca perenniss
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    Lactuca perenniss
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
    Cichorieae; Lactuca.
    1 (bases 1 to 928)
  REFERENCE
    AUTHORS
      Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
      Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
      Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
      Lai,Z., Church,S., Jackson,L. and Bradford,K.
  TITLE
    Lettuce and Sunflower ESTs from the Compositae Genome Project
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  COMMENT
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    Contact: Alexander Kozik [R.W.Michelmore]
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    Tel: 1-(530)-742-1742
    Fax: 1-(530)-752-9659
    Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
    Library was sequenced at Joint Genome Institute, Walnut Creek CA,
    using ABI 3730 machines.
  FEATURES
    Location/Qualifiers

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constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"

ORIGIN
Query Match      35.0%; Score 491.6; DB 10; Length 928;
Best Local Similarity 75.7%; Pred. No. 4.7e-114;
Matches 637; Conservative 0; Mismatches 195; Indels 9; Gaps 2;

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RESULT 11
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LOCUS
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CDNA clone CLPY14207, mRNA sequence.
ACCESSION
DW090169
VERSION
DW090169.1
KEYWORDS
GI:83888089
ORGANISM
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Lactuca perennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE
1 (bases 1 to 898)
Koziak, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Dokman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Koziak [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmunsdon Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek CA,
using ABI 3730 machines.
FEATURES
Location/Qualifiers
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(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
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Best Local Similarity 76.8%; Pred. No. 2e-112;
Matches 621; Conservative 0; Mismatches 179; Indels 9; Gaps 2;

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Cichorieae; Lactuca.
1 (bases 1 to 893)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
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Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
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http://compgenome.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Department of Vegetable Crops, R.W. Michelmore Lab  
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Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.

Location/Qualifiers  
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genotype. cDNAs were then size-fractionated, directionally  
cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>

ORIGIN

Query Match 34.4%; Score 483.4; DB 10; Length 893;  
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**TITLE**  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compgenomics.ucdavis.edu/>  
**JOURNAL**  
Unpublished (2002)  
**COMMENT**  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.  
**FEATURES**  
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/note="Vector: pBRCDNASFIAB; The standard library was  
constructed from multiple sources of RNA from a single  
genotype. cDNAs were then size-fractionated, directionally  
cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>"

## ORIGIN

Query Match 34.2%; Score 481.2; DB 10; Length 919;  
Best Local Similarity 75.8%; Pred. No. 2.1e-111;  
Matches 637; Conservative 0; Mismatches 193; Indels 10; Gaps 3;

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ACCESSION DW096275.1 GI:83894195  
VERSION DW096275  
KEYWORDS EST.  
SOURCE Lactuca perennis  
ORGANISM Lactuca perennis  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
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1 (bases 1 to 908)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
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Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compgenomics.ucdavis.edu/>  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]  
Library was sequenced at Joint Genome Institute, Walnut Creek CA,  
using ABI 3730 machines.  
**FEATURES**  
Location/Qualifiers  
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/organism="Lactuca perennis"  
/mol\_type="mRNA"  
/strain="PI-274378"  
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/note="Vector: pBRCDNASFIAB; The standard library was  
constructed from multiple sources of RNA from a single  
genotype. cDNAs were then size-fractionated, directionally  
cloned into a custom medium-copy vector and  
transformations made with three size classes  
(X-large, Y-medium and Z-small) to minimize size bias due  
to differential transformation efficiency. Details of  
each source of RNA and library construction can be  
obtained at <http://cgdb.ucdavis.edu/>"  
**ORIGIN**  
Query Match 34.2%; Score 480.8; DB 10; Length 908;



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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)  
8285.225 Million cell updates/sec

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Scoring table: IDENTITY NUC  
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Searched: 2335898 seqs, 88391439 residues

Total number of hits satisfying chosen parameters: 4671796

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Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 464.2 | 33.0          | 1647   | 8     | US-11-216-545-4819    |
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| 36   | 230.2 | 16.4 | 620  | 7 | US-11-292-078-8768   | Sequence 8768, Ap |
| 37   | 218   | 15.5 | 592  | 7 | US-11-292-078-12636  | Sequence 12636, A |
| 38   | 211   | 15.0 | 590  | 7 | US-11-292-078-8217   | Sequence 8217, Ap |
| 39   | 205.2 | 14.6 | 1177 | 6 | US-10-449-902-4008   | Sequence 4008, Ap |
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## ALIGNMENTS

## RESULT 1

US-11-369-993-3

Sequence 3, Application US/11369993

Publication NO. US20060191042A1

GENERAL INFORMATION:

APPLICANT: Fillatti, Joanne, J.

TITLE OF INVENTION: Nucleic Acid Sequences and Methods of Use for the Production of Polyunsaturated Fatty Acids

FILE REFERENCE: 16518.056

CURRENT APPLICATION NUMBER: US/11/369,993

CURRENT FILING DATE: 2006-03-08

PRIOR APPLICATION NUMBER: US/10/176,149

PRIOR FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/151,224

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: US 60/172,128

PRIOR FILING DATE: 1999-12-17

PRIOR APPLICATION NUMBER: US 09/638,508

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 6220

TYPE: DNA

ORGANISM: Glycine max

US-11-369-993-3

Query Match 33.2%; Score 467; DB 7; Length 6220;

Best Local Similarity 62.4%; Pred. No. 2e-90;

Mismatches 750; Conservative 0; Mismatches 445; Indels 6; Gaps 1;

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; Publication No. US20060135758A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaire, Paul L
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Soybeans
; FILE REFERENCE: 38-21 (53659)B
; CURRENT APPLICATION NUMBER: US/11/216,545
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: US 60/606,062
; PRIOR FILING DATE: 2004-08-31
; NUMBER OF SEQ ID NOS: 8783
; SOFTWARE: PatentIn version 3.2
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; US-11-216-545-4819
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Query Match 33.0%; Score 464.2; DB 8; Length 1647;
Best Local Similarity 62.3%; Pred. No. 5.8e-90;
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; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52711
; LENGTH: 1517
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)..(1517)
; OTHER INFORMATION: Ceres Seq. ID no. 15177298
US-11-056-355B-52711

Query Match 32.9%; Score 462.6; DB 9; Length 1517;
Best Local Similarity 62.2%; Pred. No. 1.3e-89;
Matches 748; Conservative 0; Mismatches 449; Indels 6; Gaps 1;

QY 24 TCAGTGTTCGACCGCAATCCAGGCAATTTCTTAATTTGGATTTTCAGAAATCTGGGAGAG 83
Db 40 TCTGTGGCTCTCAACAAACATCTCGTCCACACTTTCAGATTTGTGTGAAGATGGGGCGG 99
QY 84 GTAGCAGAATGTGGATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 143
Db 100 GTGGCCGAACGTGATGTTCTCTCTGCAACAGGAAGTCAGAGGTTGACCTTTGAAGCGGG 159
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QY 144 CCCGATTTGATCCGGCGCCATTTCTCGTTAAGTATCTAAAGAAACAATCCCTGCACATT 203
Db 160 TGCCATTTTGAAGAACTCCATTTAGTCTCAGCCAAATCAAGAAAGTCAATTCACCTCACT 219
QY 204 GCTTCGGCGGATCCGGCGCTCTGGTCTATCTGCTAGCTAGTTCCAGGATCTCATTTATCACT 263
Db 220 GTTTCACGGTCTCTGTTTTCGCTCATTTCTCTATGTTGTTTACGACCTCACCATTAGCT 279
QY 264 TCTTTTATACACGGTCCGCCAACACCTATCTTCCTCCTCCTCCTCCTCCTCCTCCTCCT 323
Db 280 TCTGCTCTATTTATGTTGCCACCCATTTCTCCACCTCTCTCCAGCCCTCTCTCTTTCT 339
QY 324 TAGCATGCGCGGTTTACTGGTTTTCGCAATCTTGCACTCTCTCCTCTCTCTCTCTCTCTCG 383
Db 340 TGGCATGCGCAATCTACTTGGGCTGTCCAAGGTTGCATCTTACTCGAGTTTGGGTCATTG 399
QY 384 GCCATGAATGGGCCCATCATGCTTTTAGTGTAGTACAGTGGATTTGATACGCGCTGGAT 443
Db 400 CCCATGATGTGGCCACCATGCAATTCAGTGACTACAGTTGCTTGATGATATGTTGGCC 459
QY 444 TCGTCTCTCATTCGGCTCTCTCTCACCCCTTACTTTTCTTGGAAATACAGCCATCGAAAGC 503
Db 460 TTGTCTCTCACTCCGGTCTCTCTAGTCCCATCTTTTTCATGGAATACAGCCATCGCCGTC 519
QY 504 ACCATGCAAAACAAATTTCACTCGAAACAGAGAAAGTTTATCATTTCTGTAGAACTCAGTCCC 563
Db 520 ACCACTCCAACTGCTTCTTGTAGCGGATGAAGTATTTGTGCAAAAGCAGAAAGTCTCT 579
QY 564 AGCTCAGGACTTACTCCACATACGAATTTCTTGCAACACGCTGCTGCAATCTCATCT 623
Db 580 GTATCAAGTGGTACTTAATAATAC-----CTTAAACAATCTCCAGCAGAGTCTCTCACTC 633
QY 624 TGGTCATCATGTTAACTTTAGGATTTCTTTTATATCTCTTAAACGAATGTTTCAGGCAAGA 683
Db 634 TTGCTGTACCTCTCACATTTGGTGGCCCTTGTACTTGGCTTTAAATGTTTCTGGAAGGC 693
QY 684 AGTACGATAGATTTACCAACCACTTTGTATGATGATGATGATGATGATGATGATGATGATG 743
Db 694 CTTATGATAGATTTGCTTGGCCACTATGACCCATATGCTGCTCCATTTACTCTGATCGTGAAC 753
QY 744 GAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGCGAGTGTTCAGGACCTCAAGTTTC 803
Db 754 GACTTCAATATATATATATATATATATATATATATATATATATATATATATATATATAT 813
QY 804 TTGTACAAACAAAGGATTTGGTGGTATGATGATGATGATGATGATGATGATGATGATGATG 863
Db 814 TTGCCATGCAAAAGGACTTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
QY 864 TGAATTCCTTCATTATCGTAATCATTATCTGCAACACACATCTGTGCTCACCCCAAT 923
Db 874 TCAATGGATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933
QY 924 AGATTCAACCAATGGAAGTGAATGGAAGTGAATGGAAGTGAATGGAAGTGAATGGAAGT 983
Db 934 ACACTTCTCTGAGTGGGAGCTGTTGAGAGGAGCTTTAGCAACAGTGGATGAGATTTATG 993
QY 984 GTCTCTGAATCGGTTTCCACGAGTTTACACACACACACACACACACACACACACACAC 1043
Db 994 GAATCTGGAACAGGTTCTTCCATATATATATATATATATATATATATATATATATATAT 1053
QY 1044 CCTACATTCACATTTATCATGCAAGGAGGCAAGCGAGGCCATCAAGCCCAATCTTGGGTG 1103
Db 1054 CCACATGCCACATTTATCATGCAATGGAGCTTACAAAGGCAATAAAGCCATTTTGGGAG 1113
QY 1104 ATTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATGTGGAGAGGCAAGGAAT 1163
Db 1114 AGTATTTATCGGTTTGATGAGACTCCATTTGTCAAGGCAATGTGGAGAGGCAAGAGAT 1173
QY 1164 GCATTTACATCGACGAGATGACAGCAGCAAGCAACAAAGGACATATTTGGTACCATAAAA 1223
Db 1174 GTATTTATGTGGAGCCAGATCAAGTACCGAGAGCAAGGTTGTATTTTGGTACAAATA 1233
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; NAME/KEY: misc.feature
; LOCATION: (1)..(1451)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
; OTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-355B-39927

Query Match      30.3%; Score 426.2; DB 9; Length 1451;
Best Local Similarity 61.0%; Pred. No. 7.5e-82;
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

QY 65 TTCAGAAATCTGGAGAGGTAGCAGAAATGTCGGATTTCATATCATGATCGAATGAAGAT 124
Db 144 TCAGAAACATGGGTTCAGGTGGAAGATGCGGGTTCCTACTTCTTCCAGAAATCGGAA 203
QY 125 CATGATATGGACGAAACGAGCCCGATTGATCCGGCGCCATTCCTGTTAAAGTGAATCAAAG 184
Db 204 ACCGACACCAAAAGCGTGGCGTGGAGAAACCGCCTTCTCGGTGGAGATCTGAAG 263
QY 185 AAGCAATCCCTGCAATTCCTCCGGCGATCCGGCGTCTGTFCTATCTCTGCTACGTAGTT 244
Db 264 AAAGCAATCCCGCGCATTTGTTTCAAACGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 323
QY 245 CAGGATCTCATTTATCACTCTCTTTTATACAGGTGCGCAACACCTACATTCCTCACCTC 304
Db 324 AGTGACATCATTTATAGCTCTCTTCTACTAGTCGCCACCAATTAATCTCTCTCTCTC 383
QY 305 CTCTCTCTCTAGTTTACTTAGCATGGCGGTTTACTGGTGTGTTGTCCTTCCAAATCTTGCACTCTC 364
Db 384 CTCTAGCTCTCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 443
QY 365 ACTGGTTTATGGTCTCTCGGCCATGAATGGGCCATCATGCCCTTTAGTGAGTACCAAGTG 424
Db 444 ACTGGTATCTGGTCTATAGCCACGAATGCGGTCCACGACATTCAGCGACTACCAATGG 503
QY 425 ATTGATAACGCGGTGGATTCGCTCTCAATTCGGCTCTCTCTACCCCTTACTTTCTCTGG 484
Db 504 CTGGATGACACAGTTGGTCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 563
QY 485 AAATACAGCATCGAAAGACCATGCAAAACACAAATTCATCTGAAACGAGGAAGTTTAC 544
Db 564 AGATATAGTATCGCGCTCACCATTCCAACTGGAATTCCTCGAAAGATGAAGTATTT 623
QY 545 ATTCTTAGAATCCAGTCCAGCTCAGGACTTACTCCACATACAGAAATTTCTTGACAAACG 604
Db 624 GTCCCAAGCAGAAATCAGCAATCAAGTGTACGGGAATAC-----CTCAACACCCCT 677
QY 605 CTGTGTGAATCTCTATCTTGTGTATCATGTTAACTTAGATTTCTTTTATACCTTTA 664
Db 678 CTGGACGATCATGATGTTTAAACCGTCCAGTTTGTCTCGGGTGGCCCTTGACTTAGCC 737
QY 665 ACGAATGTTTCAGGCAAGAGTACGATAGATTTTACCAACCATTTTGATCCATTGAGCCCG 724
Db 738 TTTAAGCTCTCTGGCAGACGGTATGAGGGTTCGCTTGCCATTTCTTCCCAACGCTCCC 797
QY 725 ATCTTCACCGAGGTGAGCGAATCCAGGTTTCGTTATCAGATCTTGATTCGTTGCGAGTG 784
Db 798 ATCTCAATGACCGAGAACGCTCCAGATATACCTCTCTGATCGGGTATCTTAGCCGTC 857
QY 785 TTTTACGAGTCAAGTTCTTGTTACAAACAAAGAGATTTGGTTGGGTGATGTCATGTAT 844
Db 858 TGTFTTGGTCTTTACCGTTTACGCTGTGCAACAGGGATGGCCTCGATGATGCTGCTCTAC 917
QY 845 GGAGTTCCAGTATAGTCTGAATTCCTTCAATTCATGTAATCACTTATCTGACACACACA 904
Db 918 GGAGTACCGCTTCTGATAGTGAATGGTTCCTCGTCTTGATCACTTACTTTGACGACACT 977
QY 905 CATCTCTGTCACCCCATACGATTCAAACCGAATGGAATCGAATCAAAGAGCTTTGACC 964
Db 978 CATCCCTCGTTGCTCACTACGATTTATCAGAGTGGGACTGGCTCAGGGAGCTTTGGCT 1037
QY 965 ACAATCGACAGAGATTTCTGCTCTCTGAATTCGGGTTTTTCCAGCATGTTTACACACCCAC 1024
Db 1038 ACGGTAGACAGAGACTACGGAATCTTTGAAACAGGTGTTTCCAAACATTTACAGACACAC 1097
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QY 1025 GTGTTGCCACCAATTTGTTTCCCTTACATTTCCACATTTATCATGAAAGGAGCAAGCGAGCC 1084
Db 1098 GTGGCTCATCACTGTTCTCGCAATGCGCATTTATAAGCAATGGAAGCTACAAAGGCG 1157
QY 1085 ATCAAGCCCAATCTTGGGTGATTTACAGGATGATCGACAGGACTCCATTTTTCAAAGCAATG 1144
Db 1158 ATAAAGCCCAATTTCTGGGAGACTATTTACCAGTTTCGATGGAACACCGGTGGTATGTAGCGATG 1217
QY 1145 TCGAGAGAGGCCCAAGAAATGCAATTTTACATCGAGCAAGATGACAGACAGCAAAAGG 1204
Db 1218 TATAGGAGGCAAGAGAGTGTATCTATGTAGAACCGGACAGGAAGGTGACAAAGGT 1277
QY 1205 ACATATTTGGTACCATAAAATGTAAT 1229
Db 1278 GTGTACTGGTACACAATAAGTTAT 1302

RESULT 6
US-11-056-355B-98545
; Sequence 98545, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98545
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1459)
; OTHER INFORMATION: Ceres Seq. ID no. 13600976
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1459)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
; OTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-355B-98545

Query Match      30.3%; Score 426.2; DB 9; Length 1459;
Best Local Similarity 61.0%; Pred. No. 7.5e-82;
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;
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Db 452 ACTGGTATCTGGTTCATAGCCCAAGATGGGTCCACGACGATTCAGCGATACCAATGG 511  
Qy 425 ATTGATAACGGCGTTGGATTCGTCTCCATTCGGGTCTCCCTCACCCTTACTTTTCTTGG 484  
Db 512 CTGGATGACACAGTTGGTCTTATCTTCCATTCCTTCTCTCTCTCTCTCTCTCTCTCT 571  
Qy 485 AAATACAGCCATCGAAGCAACATCGAAGCAACAAATTCACCTCGAAGCAAGAGTTTAC 544  
Db 572 AAGTATAGTATCGCGGTGACCAATTCACCACTGGATCCCTCGAAGAGATGAAGTATTT 631  
Qy 545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACG 604  
Db 632 GTCCAAAGCAGAAATCAGCAATCAAGTGGTAGCGGAATAC-----CTCAACACCT 685  
Qy 605 CTGGTCAAGTCTCATCTTGGTCAATCAATGTAACCTTAGGATTTCTTTTACCTTTTA 664  
Db 686 CTGGACGCATCATGATGTTAAACGTCAGTTGTCTCGGTGGCCCTTGTACTTAGCC 745  
Qy 665 ACGAATGTTTCAGGCAAGAGTACGATGATTTACCAACCACTTTGATCCATTCGAGCCG 724  
Db 746 TTTAACGCTCTCGGCAGACCGTATGACGGGTTCGCTTGCCATTTCTCCCAACGCTCCC 805  
Qy 725 ATCTTACCGCGTGGAGCAATCAGGTTCGGTTATCAGATCTTGGTATCGTTGCAGTG 784  
Db 806 ATCTAATAGACCGGAGACGCTCCAGATATACCTCTCTGATCGGGTATTTAGCCGTC 865  
Qy 785 TTTTACGACCTCAAGTTCTTGTGTAACAAACAAAGAGTTGGTGGGTGATGTCATGAT 844  
Db 866 TGTTTGGTCTTTACCGTTACGCTGCTGCACAAAGGATGGCCTCGATGATCTGCCCTTAC 925  
Qy 845 GGAGTTCAGTGATAGGTCTGAAATTCCTTCAATTCGTTAATCACTTATCTGCACACACA 904  
Db 926 GGAGTACCGCTTCTGATAGTGAATCGTTCCTCGTCTTGTATCACTTCTTGAGCACACT 985  
Qy 905 CATCTGTGCTCACCCCATTAAGATTAACACCAAGTGGAACTGGATCAAAAGGACCTTGACC 964  
Db 986 CATCCTCTGTTGCCCTCACTACGATTCATCAGATGGGACTGGCTCAGGGAGCTTTGGCT 1045  
Qy 965 ACAATCGACAGAGATTTCCGCTCTCTGAAATCGGTTTTCACGAGCTTTACACACACCAC 1024  
Db 1046 ACCGTAGACAGAGACTAGGAATCTTGAACAAAGTGTTCACAAATTCACAGACACACAC 1105  
Qy 1025 GTGTTGACCACTTGTTCCTTACATTCACATTCATCATGCAAGGAGGCAAGCGAGGCC 1084  
Db 1106 GTGGCTCATCACTGTTCTCGACAAATGCGCAATTAACGCAATGGAAGCTACAAAGGCG 1165  
Qy 1085 ATCAAGCCAACTCTGGGTGATTAAGGATGATCGACAGGACTCCCATTTTTCAAAGCAATG 1144  
Db 1166 ATAAAGCCAAATCTGGGAGACTTATACCAAGTTTCGATGGAAACACCGTGTATGTAGCGATG 1225  
Qy 1145 TGGAGAGGCGCAAGAAATGCAATTTACATCGAGCAAGATGCAAGCAAGCAAGAGG 1204  
Db 1226 TATAGGAGGCAAGAGGATGATCTATCTATGTAGAACCGGACAGGAAAGGTGACAAAGAGGT 1285  
Qy 1205 ACATATTGGTACCAATAAATGTAAT 1229  
Db 1286 GTGTACTGGTACAAATAAGTTAT 1310

RESULT 7  
US-11-056-355B-109784  
; Sequence 109784, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190

; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 109784  
; LENGTH: 1459  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1459)  
; OTHER INFORMATION: Ceres Seq. ID no. 13600976  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1459)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298  
; OTHER INFORMATION: as cited in SEQ ID NO 52711  
US-11-056-355B-109784

Query Match 30.3%; Score 426.2; DB 9; Length 1459;  
Best Local Similarity 61.0%; Pred. No. 7.5e-82;  
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;  
Qy 65 TTGAGAAATCTGGAGAGGTAGCAGAAATGTCGGAATTCATATGATGATCGAATGAAGAT 124  
Db 152 TCCAGAAACATGGTGCAGGTGGAGAAATGCGGTTCCTACTTCTTCCAGAAATCGAA 211  
Qy 125 CATGATATGACGAAACAGCCCGATTTGATCCGGCGCATTCCTGTTAAGTGATCTAAAG 184  
Db 212 ACCGACACCAAAAGCGGTGCGGTGCGAGAAACCGCTTCTCGGTGGAGATCTGAAG 271  
Qy 185 AAAGCAATCCCTGCACATTTGCTCCGGCGATTCGCGCTCTGGTCTATCTCTGCTAGTGT 244  
Db 272 AAAGCAATCCCGCGCATTTGTTTCAAACGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 331  
Qy 245 CAGATCTCAATATCACCTTCTTTTATACAGGTGCGCAACACTATCATTCCTCACCTC 304  
Db 332 AGTGACATCATTTATAGCTCATGCTTCTACTACGTGCGCACCAATTAATCTCTCTCTC 391  
Qy 305 CCTCCTCTCTAGTTTACTTAGCATGCGCGTTTACTGGTTTTCGCAATCTTGCATCTC 364  
Db 392 CCTCAGCTCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGCTTA 451  
Qy 365 ACTGGTTTATGGGCTCTCGGCATGAATGGCGCATCATGCTTTTAGTGATACAGTGG 424  
Db 452 ACTGATCTGGGTTCATAGCCCAAGATGGGTCAACAGCATTCAGGACTTACCAATGG 511  
Qy 425 ATTGATAACGGCGTTGGATTCGTCTCTCATTTGGCTCTCTCACCCTTACTTTTCTTGG 484  
Db 512 CTGGATGACACAGTTGGTCTTATCTTCCATTTCTTCTCTCTCTCTCTCTCTCTCTGG 571  
Qy 485 AAATACAGCCATCGAAGCAACATCGAAGCAACAAATTCACCTCGAAGCAAGAGTTTAC 544  
Db 572 AAGTATAGTATCGCGGTGACCAATTCACCACTGGATCCCTCGAAGAGATGAAGTATTT 631  
Qy 545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACG 604  
Db 632 GTCCAAAGCAGAAATCAGCAATCAAGTGGTAGCGGAATAC-----CTCAACACCT 685  
Qy 605 CTGGTCAAGTCTCATCTTGGTCAATGATGTTAACTTACCTTAGGATTTCTTTTACCTTTA 664  
Db 686 CTGGACGCATCATGATGTTAAACGTCAGTTGTCTCTCGGTGGCCCTTGTACTTAGCC 745  
Qy 665 ACGAATGTTTCAGGCAAGAGTACGATGATTTACCAACCACTTTGATCCATTCGAGCCG 724  
Db 746 TTTAACGCTCTCGGCAGACCGTATGACGGGTTCGCTTGCCATTTCTCCCAACGCTCCC 805  
Qy 725 ATCTTACCGCGTGGAGCAATCAGGTTCGGTTATCAGATCTTGGTATCGTTGCAGTG 784  
Db 806 ATCTAATAGACCGGAGACGCTCCAGATATACCTCTCTGATCGGGTATTTAGCCGTC 865  
Qy 785 TTTTACGACCTCAAGTTCTTGTGTAACAAACAAAGAGTTGGTGGGTGATGTCATGAT 844  
Db 866 TGTTTGGTCTTTACCGTTACGCTGCTGCACAAAGGATGGCCTCGATGATCTGCCCTTAC 925

QY 845 GGAGTTCAGTGAAGTCTGAATTCCTTCATATTCGTAATCACTTATCTGCACACACA 904  
DB 926 GGAGTACCGCTTCTGATAGTGAATGGTTCCTCGTCTTGATCACTTACTTGCAGCACACT 985  
QY 905 CATCTGCTGTCACCCATTACGATTCACACCGAATGGAATCGGATCAAGAGCCTTGACC 964  
DB 986 CATCCCTCGTGGCTCACTACGATTCATCAGAGTGGAGTGGCTCAGGAGAGCTTGGCT 1045  
QY 965 ACAATCGACAGAGATTCGGTCTCTGAAATCGGGTTTCCAGCAGCTTACACACCCAC 1024  
DB 1046 ACCGTAGACAGAGACTACCGAATCTTGAACAAGGTGTTCCACAACATTACAGACACACAC 1105  
QY 1025 GTGTTGCACATTTGTTCCCTACATTCACATTCATGCAAGAGGAGGAGCGGCC 1084  
DB 1106 GTGGCTCATCAGCTGTTCTCGACAATGCGGCATTTAAGCGCAATGGAAGCTACAAGGG 1165  
QY 1085 ATCAAGCCAACTCTGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATG 1144  
DB 1166 ATAAAGCCAAATCTGGAGACTATTACCAAGTTGATGGAAACCGTGGTATGTAGCGATG 1225  
QY 1145 TGGAGAGAGGCCAAGGAATGCAATTTACATCGAGCAAGATGCGACAGCAAGCAAAAGG 1204  
DB 1226 TATAGGAGGCAAGAGGTATCTATGTAGAACCGGACAGGAGGTGCAAGAAAGGT 1285  
QY 1205 ACATATTGTACATTAATATGTAAT 1229  
DB 1286 GTGTACTGTACAACAATAAGTTAT 1310

## RESULT 8

US-10-547-086-17  
; Sequence 17, Application US/10547086  
; Publication No. US20060195919A1  
; GENERAL INFORMATION:  
; APPLICANT: CropDesign N.V.  
; TITLE OF INVENTION: Arabidopsis promoters  
; FILE REFERENCE: CD-075-PCT  
; CURRENT APPLICATION NUMBER: US/10/547,086  
; CURRENT FILING DATE: 2005-08-26  
; PRIOR APPLICATION NUMBER: EP 03075587.0  
; PRIOR FILING DATE: 2003-02-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 17  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: TC160765 (PRO0193)  
US-10-547-086-17

Query Match 30.3%; Score 426.2; DB 6; Length 1617;  
Best Local Similarity 61.0%; Pred. No. 7.7e-82;  
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;  
QY 65 TTTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGATTTCATATGATGATCGAATGAAAGAT 124  
DB 149 TCAGAAACATGGTGCAGGTGGAAGATGCCGGTTCCTACTTCTTCCAGAAATCGGAA 208  
QY 125 CATGATATGGACGAACAGCCCGGATTTGATCCGGCGCCATTCGTTAAAGTATCTTAAAG 184  
DB 209 ACCGACACCAAAAGCGTGTGGCGTGGAGAAACCGCCCTTCTCGGTGGAGATCTGAAG 268  
QY 185 AAAGCAATCCCTGCATATGCTTCCGGCGATCGCGCTGTCATCTCTGCTACGTAGTT 244  
DB 269 AAAGCAATCCCGCGATTTGTTTCAAACGCTCAATCCCTCGCTCTTCTCTACCTTATC 328  
QY 245 CAGGATCTCATATACCTTCTCTTTTATACAGGTGCGCAACACCTTACATTTCTCACCTC 304  
DB 329 AGTGACATCATATAGCCCTCATGCTTCTACTAGTCGCCCAAAATTAATCTTCTCTCTC 388  
QY 305 CCTCCTCCTCTAGTTTACTTAGCATGGCGGTTTACTGGTTTTTGGCAATCTTGCATCCTC 364

## RESULT 9

US-11-056-355B-75573  
; Sequence 75573, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby

DB 399 CCTCAGCCTCTCTCTTACTTGGCCACTCTATTGGGCTCTGTCAGAGCTGTGTCTCTA 448  
QY 365 ACTGCTTTATGGTCTCTCGGCATGAATCGGCCCATCATGCTCTTATGAGTACAGTGG 424  
DB 449 ACTGCTATCTGGTCTATAGCCCAAGATCGGTACACGCAATTCAGGAGCTACCAATGG 508  
QY 425 ATTGATAACGCCGTTGGATTCGTCCTCATTCGGCTCTCTCACCCTTACTTTTCTTGG 484  
DB 509 CTGGATGACACAGTTGGTCTTATCTTCCATTCCTCTCTCTCTCTCTCTCTCTCT 568  
QY 485 AAATACAGCCATCGAAACACCATCAACACAAATTCACCTCGAAACGAGGAAGTTTAC 544  
DB 569 AAGTATAGTCACTGCGCGTCACCATTCACACACTGGATCCCTCGAAAGAGATGAAGTATT 628  
QY 545 ATTCTCTAGAACTCAGTCCAGCTCAGAGCTTACTCCACATACGAATTTCTTGACAAACAG 604  
DB 629 GTCCCAAGACGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACAAACCT 682  
QY 605 CTTGTGCAATCCTCATCTTGGTCAATCATGTTAACTTAGGATTTCTTTATACCTCTTA 664  
DB 683 CTTGGACGCATCATGATGTTAACTGTCAGTCTGCTCGGGTGGCCCTTGTACTTAGCC 742  
QY 665 ACGAATGTTTCAGGCAAGAGTACGATAGATTTCACCAACACTTTGATCCATTTGAGCCG 724  
DB 743 TTTAACGCTCTTGGCAGACCGTATACGGGTTTCGGTTCGCTCATTTCTTCCCAACGCTCCC 802  
QY 725 ATCTTTCACGCGGTGAGCGAATCCAGGTTGGTGTATCAGATCTTGGTATCTGTCAGTG 784  
DB 803 ATCTACATGACCGAGAGACGCTCCAGATATACCTCTCTGATCGGGTATTTCTAGCCGTC 862  
QY 785 TTTTACGACCTCAAGTTCTTGTGTAACAAACAAAGATTTGGTGGGTGATGTCATGTAT 844  
DB 863 TGTCTTGGTCTTTACCGTTACGCTGTCGACAAAGGATGGCTCGATGATCTGCTCTAC 922  
QY 845 GGAGTTCAGTGAAGTCTGAAATTCCTTCAATTCGTAATCACTTATCTGCACACACA 904  
DB 923 GGAGTACCGCTTCTGATAGTGAATGCGTTCCTCTTGTATCACTTACTTGCAGCACACT 982  
QY 905 CATCTGCTGTCACCCCATTCAGATTCAACCGAATGGAATCGAATCAAGAGAGCTTGACC 964  
DB 983 CATCCCTGTTGGCTCACTACGATTCATCAGATGGAGTGGCTCAGGAGAGCTTGGCT 1042  
QY 965 ACAATCGACAGAGATTCGGTCTCTGAAATCGGGTTTCCAGCAGTTTACACACACCCAC 1024  
DB 1043 ACCGTAGACAGAGACTACGGAATCTTGAACAGGTGTTCCACAAATTCAGACACACAC 1102  
QY 1025 GTGTTGCACCATTTGTTTCCCTACATTCACATTCATGCAAGAGGAGGAGGAGGAGCC 1084  
DB 1103 GTGGCTCATCACCTGTTCTCGCAATTCGCGCAATTAACGCAATGGAAGCTACAAGGG 1162  
QY 1085 ATCAAGCCAACTCTGGGTGATTTACAGGATGATCGACAGACTCCATTTTCAAAGCAATG 1144  
DB 1163 ATAAAGCAATTCCTGGAGACTATTACAGTTTCGATGGAACCGTGGTATGTAGGATG 1222  
QY 1145 TGGAGAGAGGCCAAGGAATGCAATTTTACATCGAGCAAGATGCAAGCAAGCAAAAGG 1204  
DB 1223 TATAGGAGGCAAGAGGATGATCTATGTAGAACCGGACAGGAGGTGCAAGAAAGGT 1282  
QY 1205 ACATATTGGTACCAATAAATGTAAT 1229  
DB 1283 GTGTACTGTACAACAATAAGTTAT 1307







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Db 686 CTTGACGCATCATGATGTTAAACGTCAGTTTGTCTCGGGTGGCCCTTGTACTTAGCC 745
Qy 665 ACGAATGTTTTCAGGCAAGAGTACGATAGATTACCAACCACTTTGATPCCATTGAGCCG 724
Db 746 TTTAAAGCTCTCGGCAGACCGTATGACGGGTTGCGTTGCCATTCTTCCCAACGCTCCC 805
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; Publication No. US20060150283A1
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; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
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; FEATURE:
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; LOCATION: (1)..(1411)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
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; US-11-056-355B-32464
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; APPLICATION NUMBER: US/11/340,318
; FILING DATE: 26-JAN-2006
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,608
; FILING DATE: 08-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,650
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lundquist, Ronald C.
; REGISTRATION NUMBER: 37,875
; REFERENCE/DOCKET NUMBER: 07148/042002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/335-5070
; TELEFAX: 612/288-9696
; INFORMATION FOR SEQ ID NO: 1:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
; FEATURE:
; OTHER INFORMATION: Wild type F form.
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; Publication No. US20060137040A1
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; APPLICANT: DeBonte, L. et al.
; TITLE OF INVENTION: CANOLA OIL HAVING INCREASED OLEIC ACID AND
; DECREASED LINOLENIC ACID CONTENT
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/340,318
; FILING DATE: 26-JAN-2006
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,608
; FILING DATE: 08-AUG-1997
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/675,650  
FILING DATE: 03-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Lundquist, Ronald C.  
REGISTRATION NUMBER: 37,875  
REFERENCE/DOCKET NUMBER: 07148/042002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/335-5070  
TELEFAX: 612/288-9696  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 base pairs  
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HYPOTHETICAL: NO  
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ORGANISM: Brassica napus  
FEATURE:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 7          | 665.6 | 47.3        | 1134   | 10 | US-10-912-534-33  |
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| 19 | 486.4 | 34.6 | 1134 | 10 | US-10-912-534-29     | Sequence 29, Appl  |
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| 23 | 467   | 33.2 | 6220 | 8  | US-10-465-800-3      | Sequence 3, Appli  |
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| 25 | 462.6 | 32.9 | 1586 | 8  | US-10-425-114-14778  | Sequence 14778, A  |
| 26 | 462.6 | 32.9 | 2931 | 8  | US-10-424-599-123945 | Sequence 123945, A |
| 27 | 459.8 | 32.7 | 1457 | 8  | US-10-425-114-12782  | Sequence 12782, A  |
| 28 | 430.6 | 30.6 | 1152 | 8  | US-10-772-227-7      | Sequence 7, Appli  |
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| 40 | 417.2 | 29.7 | 1164 | 10 | US-10-912-534-1      | Sequence 1, Appli  |
| 41 | 412.8 | 29.4 | 1411 | 3  | US-09-852-399-3      | Sequence 3, Appli  |
| 42 | 411   | 29.2 | 1164 | 8  | US-10-772-227-30     | Sequence 30, Appl  |
| 43 | 411   | 29.2 | 1164 | 10 | US-10-912-534-30     | Sequence 30, Appl  |
| 44 | 411   | 29.2 | 1200 | 10 | US-10-912-534-129    | Sequence 129, App  |
| 45 | 407   | 28.9 | 2043 | 9  | US-10-739-930-3184   | Sequence 3184, Ap  |

## ALIGNMENTS

RESULT 1  
 US-10-622-774-1  
 ; Sequence 1, Application US/10622774  
 ; Publication NO. US2005002270A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Kentucky Research Foundation  
 ; APPLICANT: Hildebrand, David  
 ; APPLICANT: Hatanaka, Tomoko  
 ; TITLE OF INVENTION: RECOMBINANT STOKESIA EPSYGENASE GENE  
 ; CURRENT APPLICATION NUMBER: US/10/622,774  
 ; CURRENT FILING DATE: 2003-07-21  
 ; PRIOR APPLICATION NUMBER: 60/396,406  
 ; PRIOR FILING DATE: 2002-07-19  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 1406  
 ; TYPE: DNA  
 ; ORGANISM: Stokesia laevis  
 US-10-622-774-1

|                       |                 |   |           |              |
|-----------------------|-----------------|---|-----------|--------------|
| Query Match           | 100.0%          | Score 1406;   | DB 9;     | Length 1406; |
| Best Local Similarity | 100.0%          | Pred. No. 0;  |           |              |
| Matches 1406;         | Conservative 0; | Mismatches 0;   | Indels 0; | Gaps 0;      |
| QY                    | 1               | GTAGGTTTGGGTGTCGGTGCAGTTCGACCGGAATCCACGCAATTTCTAATTT        | 60        |              |
| Db                    | 1               | GTAGGTTTGGGTGTCGGTGCAGTTCGACCGGAATCCACGCAATTTCTAATTT        | 60        |              |
| QY                    | 61              | CGATTTTCAGAAATCTGGGAGAGGTAGCAGATGTCGGATTCATATGATGATCGAATGAA | 120       |              |
| Db                    | 61              | CGATTTTCAGAAATCTGGGAGAGGTAGCAGATGTCGGATTCATATGATGATCGAATGAA | 120       |              |
| QY                    | 121             | AGATCATGATATGGACGACGACCGCCGATTCATCGGCGCCATTCCTGTTAAGTGATCT  | 180       |              |
| Db                    | 121             | AGATCATGATATGGACGACGACCGCCGATTCATCGGCGCCATTCCTGTTAAGTGATCT  | 180       |              |
| QY                    | 181             | AAAGAAGCAATCCCTGCAATTCGTCGCGGATCCCGCTGTGTCATCTGCTACGTC      | 240       |              |
| Db                    | 181             | AAAGAAGCAATCCCTGCAATTCGTCGCGGATCCCGCTGTGTCATCTGCTACGTC      | 240       |              |

181 AAAGAAAGCAATCCCTGTCACATTTGCTTCGGGGATCCGCCGTCTGGTTCATCTCTGCTAGT 240  
241 AGTTCAAGGATCTATATACCTTCCTTTTATACAGGTCCCAACACCTCATCTCTCA 300  
241 AGTTCAAGGATCTATATACCTTCCTTTTATACAGGTCCCAACACCTCATCTCTCA 300  
301 CCTCCCTCCTCTAGTTTACTTAGCATGCGCGTTTACTGGTTTGGCAATCTTGAT 360  
301 CCTCCCTCCTCTAGTTTACTTAGCATGCGCGTTTACTGGTTTGGCAATCTTGAT 360  
361 CCTCACTGTTTATGGGTCTCGGCCATGAATGCGGCATCATGCTTTAGTGATACCA 420  
361 CCTCACTGTTTATGGGTCTCGGCCATGAATGCGGCATCATGCTTTAGTGATACCA 420  
421 GTGGATTGAATACGCGGTGGATTGCTCTCATTCGGCTCTCTCACCCCTTACTTTTC 480  
421 GTGGATTGAATACGCGGTGGATTGCTCTCATTCGGCTCTCTCACCCCTTACTTTTC 480  
481 TTGGAAATACAGCCATCGAAAGCACCATGCAACACAAATTCACCTCGAAACGAGGAAT 540  
481 TTGGAAATACAGCCATCGAAAGCACCATGCAACACAAATTCACCTCGAAACGAGGAAT 540  
541 TTACATTCCTAGACTCAGTCCAGCTCAGACTTACTCCACATACGAATTTCTTGACAA 600  
541 TTACATTCCTAGACTCAGTCCAGCTCAGACTTACTCCACATACGAATTTCTTGACAA 600  
601 CACGCTCGGTGGAATCCTCATCTTGGTTCATCATGTTAACTTAGGATTTCTTTATACCT 660  
601 CACGCTCGGTGGAATCCTCATCTTGGTTCATCATGTTAACTTAGGATTTCTTTATACCT 660  
661 CTTAAAGAAATGTTTCAGGCAAGATGATAGATTTTACCAACCACTTTGATCCATTGAG 720  
661 CTTAAAGAAATGTTTCAGGCAAGATGATAGATTTTACCAACCACTTTGATCCATTGAG 720  
721 CCCGATCTTCCAGGCTGAGCGAATCCAGGTTCGTTTATCAGATCTTGGTATCGTTGC 780  
721 CCCGATCTTCCAGGCTGAGCGAATCCAGGTTCGTTTATCAGATCTTGGTATCGTTGC 780  
781 AGTGTGTTTACGACCTCAAGTTTCTTGTTACAAACAAAGGATTTGGTGGTGAATGAT 840  
781 AGTGTGTTTACGACCTCAAGTTTCTTGTTACAAACAAAGGATTTGGTGGTGAATGAT 840  
841 GTATGGAGTTCAGTGATAGTCTGAATCTTCTTCAATTCGTAATCACTTATCTGCACCA 900  
841 GTATGGAGTTCAGTGATAGTCTGAATCTTCTTCAATTCGTAATCACTTATCTGCACCA 900  
901 CACACATCTGTGTCACCCCATTTAGATTTCAACCGAATGGAATCGATCAAGGAGCCTT 960  
901 CACACATCTGTGTCACCCCATTTAGATTTCAACCGAATGGAATCGATCAAGGAGCCTT 960  
961 GACCAATTCGACAGAGATTTTCGGTCTCTGTAATCGGGTTTTCACGACGTTTACACAC 1020  
961 GACCAATTCGACAGAGATTTTCGGTCTCTGTAATCGGGTTTTCACGACGTTTACACAC 1020  
1021 CCACTGTGACCAATTTGTTTCCCTACATTCGATTCATGCAAGATGCAAGGAGCCTT 1080  
1021 CCACTGTGACCAATTTGTTTCCCTACATTCGATTCATGCAAGATGCAAGGAGCCTT 1080  
1081 GGCATCAAGCAATCTTGGGTGATTTACAGGATGATCGACAGATCTCCATTTTCAAGC 1140  
1081 GGCATCAAGCAATCTTGGGTGATTTACAGGATGATCGACAGATCTCCATTTTCAAGC 1140  
1141 AATGTGGAGAGGCAAGGAATGCAATTTACATCGAGCAAGATGCAAGGAGCCTT 1200  
1141 AATGTGGAGAGGCAAGGAATGCAATTTACATCGAGCAAGATGCAAGGAGCCTT 1200  
1201 AGGACATATTTGGTACCAATAAATGTAATCGATGATGAGTTTGTGGAATATGACA 1260  
1201 AGGACATATTTGGTACCAATAAATGTAATCGATGATGAGTTTGTGGAATATGACA 1260  
1261 TGCAGCATCCCTTTGTATGCTTGAATCGTTCTATTTCTTTATGTTTGTGGAATATAA 1320  
1261 TGCAGCATCCCTTTGTATGCTTGAATCGTTCTATTTCTTTATGTTTGTGGAATATAA 1320

1321 TAAGTAAATCTTTGAGTGAAGATGGGAGCAGGAAACAAGCAGAAATATATACGCTAAA 1380  
1321 TAAGTAAATCTTTGAGTGAAGATGGGAGCAGGAAACAAGCAGAAATATATACGCTAAA 1380  
1381 AAAAAAAAAAAAAAAAAAAAAAAAAA 1406  
1381 AAAAAAAAAAAAAAAAAAAAAAAAAA 1406

RESULT 2  
US-10-622-774-9  
; Sequence 9, Application US/10622774  
; Publication No. US20050022270A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Kentucky Research Foundation  
; APPLICANT: Hildebrand, David  
; APPLICANT: Hatanaka, Tomoko  
; TITLE OF INVENTION: RECOMBINANT STOKESIA EPSOXYGENASE GENE  
; FILE REFERENCE: 050229-0377  
; CURRENT APPLICATION NUMBER: US/10/622,774  
; CURRENT FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: 60/396,406  
; PRIOR FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 1364  
; TYPE: DNA  
; ORGANISM: Veronia galamensis  
US-10-622-774-9

Query Match 61.9%; Score 870; DB 9; Length 1364;  
Best Local Similarity 86.1%; Pred. No. 7.5e-228;  
Matches 963; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

120 AAGATCATGATATGGAGCAACGAGCGCCGATTGATCCGGGCCATCTCGTTAAGTGATC 179  
149 ATGATCATATATATAAGCAACGCGTGCACCGTTGATGCGGCACCATCTCGTTAAGCGATC 208  
180 TAAAGAAAGCAATCCCTGCAATTTCTTCGGCGCATCGCGTCTGCTGATCATCTGCTACG 239  
209 TAAAGAAAGCAATCCCTGCAATTTCTTCGGCGCATCTCGCATCGTTTCATCGTGTACG 268  
240 TAGTTCAAGATCTCATATACCTTCCTTTTATACAGGTGCGCCAAACACCTACATCTCTC 299  
269 TTGTTCAAGATCTCATATATACCTTCCTTTTATACAGGTGCGCCAACTCTTACATCTCTC 328  
300 ACCTCCCTCCCTCTAGTTTACTTACATGCGCGGTTTACTGTTTTCGCAATCTTGCA 359  
329 TCTTCTCTCTCTCTACCTTACTTACATGCGCTGTTTACTGTTTTCGCAATCTTGCA 388  
360 TCCTCACTGTTTATGGGTCTCTCGGCCATGAATCGGCCATCATGCTTTCAGTGTAC 419  
389 TCCTCACTGTTTATGGGTCTTGGCCATGAATGCGCCATCATGCTTATAGTGTAC 448  
420 AGTGAATGATPAAACGCGTTGGAATGCTTCCATTCGATTCGCTCTCTCTACCCCTTACTTTT 479  
449 AGTGGGTTGATAACACCGTTGGAATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 508  
480 CTTGGAATACAGCCATCGAAGCAGCATGCAACACAAATTCACCTCGAAACGAGGAAG 539  
509 CTTGGAATACAGCCATCGAAGCAGCATGCAACACAAATTCACCTCGAAGCAGGAAG 568  
540 TTTACATTTCTTAGAATCAGTCCAGCTCAGGACTTACTTCCACATACGAATTTCTTGACA 599  
569 TTTACATTTCTTAGAAGCAAGTCCAGCTCAGGAAATCTCCAAATTTCAATTTCTTGACA 628  
600 ACAGCCTGCTGGAATCTCTATCTTGGTTCATCATGTTTAACTTAGGATTTCTTTATAC 659  
629 ACAGCCTGCTGGAATCTCTATCTTGGTTCATCATGTTTAACTTAGGATTTCTTTATAC 688  
660 TCTTAAACGAATGTTTTCAGGCAAGATGATAGATTTTACCAACCACTTTGATCCATGTA 719

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Db 689 TCTTGACCAATATTTTCAGGCAAGAAATACAAAGGTTTGCACCACTTTGATCCGTTGA 748
QY 720 GCCCGATCTTACCGAGCGTGACGGAATCCAGGTTCGGTTATCAGATCTTGGTATCGTTG 779
Db 749 GCCCATCTTCACTGAGCGTGAACGAATCCAGTCTGCTATCGGATCGGGTCTCATTTG 808
QY 780 CAGTGTTTACGAGCTCAAGTTCTTCTGTACAAACAAAGAGATTGGTTGGGTGATGCA 839
Db 809 CTGTGTTTACCGGCTTAAGTTTCTTTGTAGCGAAAAAAGGGTTCCGGTTGGGTAATCGCA 868
QY 840 TGTATGAGTTCAGAGTATAGTCTCAATTTCCCTTCAATATCGTAATCACTTATCTCCACC 899
Db 869 TGTACGGAGCCCGAGTGGTGGCTGAATGCCTTCAATAATGATCACTTATCTCCACC 928
QY 900 ACACACATCTGTCTGTCACCCCATTTAGCATTTCAACCGAATGGAATCGAATCAAGAGCCT 959
Db 929 ACACCATCTGTCTTCCGCTCATTCAGATTCGACCGAATGGAATCGAATCAAGAGCCT 988
QY 960 TGACCAATTCGACAGAGATTTCCGCTCTCTGTAATCGGTTTTCACGAGCTTACACACA 1019
Db 989 TGACTACAATCGATAGAGATTTCCGCTCTCTGTAATAGGGTGTTCATGACGTCATCTACA 1048
QY 1020 CCCACGTGTGCACCATTTGTTTCCCTACATTCACATTCATCATGCAAGAGGCAAGCG 1079
Db 1049 CACACGTGTGCATCATTTGTTTCCGCTACATTCACATTCATCATGCAAGAGGCGAGCG 1108
QY 1080 AGGCCATCAAGCCAACTTTGGGTGATTTACAGGATGATCGACAGACTCCATTTTCAAAG 1139
Db 1109 ACGCATAAAGCCGGTGTAGGGAGTATCGATGATCGATAGGACTCCGTTTACAAAG 1168
QY 1140 CAATGTGGAGAGGCGCAAGGAATGATTCATTCAGCAAGATGATGAGAGCAAGCAACA 1199
Db 1169 CAATGTGGAGAGGCGCAAGGAATGATTCATTCAGCAAGATGATGAGAGCAAGCAACA 1228
QY 1200 AAGGACATATTTGTTACCAATAATGATTAATCGATGATG 1237
Db 1229 AAGGTGATATTTGTTACCAATAATGATGATGATGATG 1266

RESULT 3
US-10-912-534-131
; Sequence 131, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Stokesia laevis B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1134)
US-10-912-534-131
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Query Match 49.6%; Score 697; DB 10; Length 1137;  
Best Local Similarity 75.8%; Pred. No. 2.5e-180;

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Matches 862; Conservative 0; Mismatches 275; Indels 0; Gaps 0;
QY 92 ATGTCGGATTCATATGATGATCAATGAAGAATCATGATATGAGCAAGACGCCGATTT 151
Db 1 ATGGCTTCTCTCTATGACGACAGAAATGAAGGACCATGATATGATGAAGAACCAATTT 60
QY 152 GATCCGGCGCCATCTCGTTAAGTATGATCTAAGAAGCAATCCCTGCACATTCGTTCCGG 211
Db 61 GACCTGCTCTCTTTCTCTTTCTGATCTTAAGAAGGCTATTTCCAGCTCATTTGCTTTA 120
QY 212 CGATCCGGCGCTCTGGTCATCTCTGCTACGCTAGTATTCAGGATCTCATTTATCACTTCCTTTTA 271
Db 121 AGATCTGCTGTTTGGTCTTCTGCTATGTTGGTGAAGACCTTATTTATTTACTTTCTTTTG 180
QY 272 TACAGGTGCGCAACACCTTACATTCCTCACCTCCCTCTCTCTCTAGTTTCTTAGCATGG 331
Db 181 TATACTGTGGCTTAACACTTATATTCACATCTTCACTCCACTTGTCTTATCTTGTCTGG 240
QY 332 CCGGTTTACTGGTTTGGCAATCTTGCATCTCTCACTGGTTTATGGTCTCTCGGCATGAA 391
Db 241 CCAGTGTATTTGGTTCTGCAATCTTGTGCACTTCTTCTGGAATTTGGGTTCTTGGACATGA 300
QY 392 TCGGCGCATCATGCTTTAGTGAATACCACTGATGATTAAGCCGCTTGGATTCGTCCTC 451
Db 301 TCGGACATCATGCTTTCTGAGTATCAATGATGATCAACGCTGTGGATTCGTCCTT 360
QY 452 CATTCGGCTCTCTCACCCCTTACTTTCTTGGAAATACAGCCATCGAAAGCAACCATGCA 511
Db 361 CATTCGCTCTTTTGAATCTTCTTCTTGAAGTATTTCTCATAGAAGCATCATGCT 420
QY 512 AACACAAATTCATCGAAACGAGGAGTTTACATTTCTAGAACTCTAGAACTCAGTCCCGCTCAG 571
Db 421 AACACTAACTCTCTTGAAGAACGAGGAGTGTATTTTCAAGAACTCAATCTCAACTTGA 480
QY 572 ACTTACTCTCACATACGAATTTCTTGAACACGCTGTGCGAATCTCTCATCTTGGTCATC 631
Db 481 ACTTATTTCTATTTAGGTTCTTCTGACAACTCTCAGGAGAAATTTCTTATTTCTTGAT 540
QY 632 ATGTTAACTTATAGGATTTCTTTATACCTCTTAAACGAATGTTTTCAGGCAAGATACGAT 691
Db 541 ATGCTTACTCTTGGATTTCCACTTTTATCTTTTGAATCTTCTGAAAGAAATATGAC 600
QY 692 AGATTTACCAACACTTTGATCCATTTGACCCGATCTTCAACGAGCGTGAGGAAATCCAG 751
Db 601 AGATTCACCTAACTTTTCAGCCACTTTCTCCAATTTTCACTGAGAGAGAGAAATTCAA 660
QY 752 GTTGGTTATCAGATCTTGGTATCGTTGAGGTTTACGGACTCAAGTTTCTTGTACAA 811
Db 661 GTTGTCTTTCTGATCTTGGAAATGTTGGCTGTGTTCTATGGACTTAAAGTTCTTGTTCAA 720
QY 812 ACAAAGGATTTGGTGGTGTATGTCATGTATGGAGTTTCCAGTGTATGAGTCTGAAATTC 871
Db 721 ACTAAGGATTTGGATGGTTATGTCATGTATGGATGTCAGTGAATGAGTCTTAACTCT 780
QY 872 TTCATTTATCGTAATCACTTATCTGCACCAACACATCTGTCTGTCACCCCATTTACGATTC 931
Db 781 TTCATTTATGATTAATCTTCTCATCATCTCATCTTCTTCTTCTCCACTTATGATTTCT 840
QY 932 ACCGATGGAATCGGATCAAGAGGCTTGAACCAATCGACAGATGATTTCCGTCCTCTG 991
Db 841 ACTGAGTGAAGTGAATGAAGGTCATTAAGGCTGATCTACTTATGACAGAGACTTCGAGCTTT 900
QY 992 AATCGGTTTTCACGACGTTTACACACACCCACGTTGTGACCATTTGTTTCCCTACAT 1051
Db 901 AACAGATGTTCCATGACGCTGACTCATCTCATGTGCTTCTCATCACTTTTCCATATAT 960
QY 1052 CCACATTTATCATGCAAGAGGCAAGCGGAGGCTCAAGCCAAATCTTGGGTGATTTACAG 1111
Db 961 CCACATTTATCATGCTAAAGGAGGCTTCTGAGGCTTATTAAGCCAAATCTTGGAGACTATA 1020
QY 1112 ATGATCGACGAGCTCCATTTTTCAAAGCAATGTTGGAGAGGCGCAAGAAATGCAATTTAC 1171
Db 1021 ATGATTTGATAGAACTCCATTTTTCAGAGGCTATGTTGGAGAGGCTTAAGGATGCTAT 1080
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| Matches 835; Conservative 0; Mismatches 229; Indels 6; Gaps 1; |   |
|--|---|
| QY 159   | CGCATCTCTGTTAGTGTCTAAAGAAAGCAATCCCTGCACATTCCTTCGGCGATCGG 218          |
| Db   |   |
| QY 71  | CACCTTTGACATTAAGTGTATATAAGAAAGCAATCCCTCCCATTCGTTCAAGCATCTG 130        |
| Db   |   |
| QY 219   | CGCTCTGGTCACTCTGCTAGTGTTCAGATCTCATATACACTTCTCTTTTATACACGG 278         |
| Db   |   |
| QY 131   | TCATAGCTTCTGCTACTATGTGTGTTTCATGATCTCATCGTCTCTCTACGTCTTCTTCTCC 190     |
| Db   |   |
| QY 279   | TCGCCAACACCTACATTCCTCACTCCCTCCCTCTCTAGTTCATTTAGCATGCGCGTTT 338        |
| Db   |   |
| QY 191   | TCGCAACGACATATATCT 250        |
| Db   |   |
| QY 339   | ACTGTTTTCGCAATCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 398      |
| Db   |   |
| QY 251   | ACTGTTTTCGCAATCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 310      |
| Db   |   |
| QY 399   | ATCATGCTCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 458      |
| Db   |   |
| QY 311   | ACCATGCTCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 370      |
| Db   |   |
| QY 459   | CT 518      |
| Db   |   |
| QY 371   | CT 430      |
| Db   |   |
| QY 519   | ATTCACTCGAAACGAGGAGTTTACATTCCTAGAACTCAGTCCCGCAGCTCAGGACTTACT 578      |
| Db   |   |
| QY 431   | ATTCACTCGAAACGAGGAGTTTACATTCCTAGAACTCAGTCCCGCAGCTCAGGACTTACT 490      |
| Db   |   |
| QY 579   | CCACATACGAATTTCTTGACACACGCTCTGTCGATCTCTCTCTCTCTCTCTCTCTCTCTCT 638     |
| Db   |   |
| QY 491   | CCA-----AAATCTCTAAACCAACCCACCTCTGGAAGGGTGTCTCTCTCTCTCTCTCTCT 544      |
| Db   |   |
| QY 639   | CCTTAGGATTTCTCTTTATACCTCTTAAACGAATGTTTTCAGGCAAGAGTACGATAGATTTA 698    |
| Db   |   |
| QY 545   | CTCTAGGGTTTCTCTTTGTTACCTGTTTAACTTAATCTCTGGAAGAAATACCAAGGTTTG 604      |
| Db   |   |
| QY 699   | CCAAACCACTTTTGATCCATTTGAGCCCGCATCTTCAACCGAGCGTGAGCGAATCCAGGTTGCGT 758 |
| Db   |   |

RESULT 6  
US-10-772-227-33  
; Sequence 33, Application US/10772227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbsky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: Klook, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: Mc Laird, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772,227  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Stokesia laevis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1131)  
US-10-772-227-33

|  |   |
|--|---|
| Query Match 47.3%; Score 665.6; DB 8; Length 1134;             |   |
| Best Local Similarity 77.1%; Pred. No. 1.1e-171;               |   |
| Matches 825; Conservative 0; Mismatches 239; Indels 6; Gaps 1; |   |
| QY 159   | CGCCATTCCTGTTAGTGTCTAAAGAAAGCAATCCCTGCACATTCCTTCGGCGATCGG 218         |
| Db   |   |
| QY 219   | CGCTCTGTCATCTCTGCTAGTGTTCAGGATCTCATATACCTTCTCTTTTATACACGG 278         |
| Db   |   |
| QY 131   | TCATAGGTCCTTCATACATATGTGTTCATGATCTCATCTCTCTCTCTCTCTCTCTCTCT 190       |
| QY 279   | TCGCCAACACCTACATTCCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 338      |
| Db   |   |
| QY 191   | TCGCAACTACATATATCT 250        |
| QY 339   | ACTGTTTTCGCAATCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 398      |
| Db   |   |
| QY 251   | ACTGTTTTCGCAATCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 310      |
| QY 399   | ATCATGCTCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 458      |
| Db   |   |
| QY 311   | ACCATGCTCTTTCGATCTCTCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 370      |
| QY 459   | CT 518      |
| Db   |   |
| QY 371   | CT 430      |
| QY 519   | ATTCACTCGAAACGAGGAGTTTACATTCCTAGAACTCAGTCCCGCAGCTCAGGACTTACT 578      |
| Db   |   |
| QY 431   | ATTCACTCGAAACGAGGAGTTTACATTCCTAGAACTCAGTCCCGCAGCTCAGGACTTACT 490      |
| Db   |   |
| QY 579   | CCACATACGAATTTCTTGACACACGCTCTGTCGATCTCTCTCTCTCTCTCTCTCTCTCTCT 638     |
| Db   |   |
| QY 491   | CCA-----AAATCTCTAAACCAACCCACCTCTGGAAGGGTGTCTCTCTCTCTCTCTCTCT 544      |
| QY 639   | CCTTAGGATTTCTCTTTATACCTCTTAAACGAATGTTTTCAGGCAAGAGTACGATAGATTTA 698    |
| Db   |   |
| QY 545   | CTCTAGGGTTTCTCTTTGTTACCTGTTTAACTTAATCTCTGGAAGAAATACCAAGGTTTG 604      |
| QY 699   | CCAAACCACTTTTGATCCATTTGAGCCCGCATCTTCAACCGAGCGTGAGCGAATCCAGGTTGCGT 758 |
| Db   |   |

Db 605 CCAACCACTTTGATCCATTTAGTCCCATCTTTCACGAGAGGAAAGGATTCAGGTCTCTG 664  
Qy 759 TATCAGATCTTGGTATCGTTCAGTGTGTTTACGAGTCAAGTCTTCTGTACAAACAAAG 818  
Db 665 TATCAGATCTTGGTCTTCTAGCTGTAACTAAGCAATCAAGCTTCTTGTCTGCTGAAAG 724  
Qy 819 GATTGTTGGTGTGATGTCATGTATGAGTGTCCAGTGTATAGGTCTGAATTCCTTTCAATTA 878  
Db 725 GAGCTGTCTGGGTGACATGCATCTATGAGTTCAGATCTTCCAGTCTAGGTGTAAGCGTGTCTTCG 784  
Qy 879 TCGTAATCACTTATCTGACACACACATCTGTCTACCCCATTAAGATTCACCCGAAT 938  
Db 785 TTTTGTATCACTTACTTGTGACACACACCTTCTTCCGTCCATTTACGATTCCTACTGAGT 844  
Qy 939 GGAATCGATCAAGAGGACCTTGACCAATCGACAGAGATTTTCGGTCTCTGATCGG 998  
Db 845 GGAATCGATCAGAGGACCTTGACCAATCGATCGATAGGATTTTGGGTCTCTAATAGG 904  
Qy 999 TTTTCCAGCTTATACACACACACCTGTTGCAACCTGTTGTTCCCTTACATTCACAT 1058  
Db 905 TTTTCCATGACCTTATACACACACCTGATGATTCATCTTGTATCTTACATTCACACT 964  
Qy 1059 ATCATGCAAGAGGACCAAGGACCTCAAGCCATCAAGCCATCTTGGTGTATACAGGATTCG 1118  
Db 965 ATCATGCAAGAGGACCAAGGATGCAATCAACCCAGTCTTGGGTGATTTATTAAGATTG 1024  
Qy 1119 ACAGGACTCCATTTTCAAGCAATGTGAGAGGACCAAGGATGCAATTTACATTCGAGC 1178  
Db 1025 ATAGGACTCTTATTTCAAGCAATGTGAGAGGACCAAGGATGCAATTTATTAAGATTG 1084  
Qy 1179 AAGATGCAAGAGGACCAAGGACATATTTGTTACCAATAAATGTAA 1228  
Db 1085 CAGATGAAGATACTGAACACAAAGGTTTACTGGTACCAATAAATGTAA 1134

## RESULT 7

US-10-912-534-33  
; Sequence 33, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbak, Michelle L.  
; APPLICANT: Baublite, Catherine E.  
; APPLICANT: Kloeck, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hreko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Deryck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; FILE OF INVENTION: PLANTS MADE THEREFROM  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Stokesia laevis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1131)  
US-10-912-534-33

Query Match 47.3%; Score 665.6; DB 10; Length 1134;  
Best Local Similarity 77.1%; Pred. No. 1.1e-171;  
Matches 825; Conservative 0; Mismatches 239; Indels 6; Gaps 1;

Qy 159 CGCAATTCGTGATGATCTTAAGAAAGCAATCCCTGACATTCCTTCGGCGATCG 218

Db 71 CACCTTTCACTTAAGTGATATATAAGAAAGCAATCCCTCCCATTTGCTTCAAAAGTCTG 130  
Qy 219 CCGTCTCGTCACTCTGCTAGTTCAGGATCTCAATTAACCTTCTCTTTTATACAGG 278  
Db 131 TCAAGAGTCTTCATATGTTTCTCATGATCTCATCGTCTCTCTAGGCTCTTCTTCTTC 190  
Qy 279 TCGCAACACTTACATTTCTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 338  
Db 191 TCGCAACTCATATATTTACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250  
Qy 339 ACTGGTTTTCCTTCT 398  
Db 251 ACTGGTTTTCCTTCT 310  
Qy 399 ATCATGCTTTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 458  
Db 311 ACCATGCTTTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370  
Qy 459 CTCTCTCTCACTTCT 518  
Db 371 CTCTCTCTCACTTCT 430  
Qy 519 ATTCACCTCGAAAGAGGAGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 578  
Db 431 ATTCACCTCGAAAGAGGAGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 490  
Qy 579 CCAATATCGAATTTCTTGAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638  
Db 491 CCA-----AAATCCTAAACAAACCTGGAAGGTTTCTCTCTCTCTCTCTCTCTCTCT 544  
Qy 639 CTTTAGATTTCTCTTATCTCTTAAAGATTTTCAGGCAAGAGTTCAGATAGATTA 698  
Db 545 CTCTAGGTTTCTCTTATCTCTTAAAGATTTTCAGGCAAGAGTTCAGATAGATTA 604  
Qy 699 CCAACCACTTTGATCTGAGCCGATCTTCAAGAGGAGTTCAGGCAAGAGTTCAGATAG 758  
Db 605 CCAACCACTTTGATCTGAGCCGATCTTCAAGAGGAGTTCAGGCAAGAGTTCAGATAG 664  
Qy 759 TATCAGATCTTGGTATCGTTCAGTGTTCAGGACTCAAGTTCCTTGTACAAACAAAG 818  
Db 665 TATCAGATCTTGGTATCGTTCAGTGTTCAGGACTCAAGTTCCTTGTACAAACAAAG 724  
Qy 819 GATTGTTGGTGTATGTCATGTATGAGTTCAGGACTCAAGTTCCTTGTACAAACAAAG 878  
Db 725 GAGCTGTCTGGGTGACATGTCATCTAGGAGTTCAGGACTCAAGTTCCTTGTACAAAC 784  
Qy 879 TCGTAATCACTTATCTGCACACACACATCTGTCTGCTCAACCCATTAAGATTCACCCGA 938  
Db 785 TTTTGTATCACTTACTTGCACACACACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 844  
Qy 939 GGAATCGATCAAGAGGACCTTGACCAATCGACAGAGATTTTCGGTCTCTGATTCGGG 998  
Db 845 GGAATCGATCAAGAGGACCTTGACCAATCGATGAGATTTTGGGTCTCTTAAATAGG 904  
Qy 999 TTTTCCAGGCTTATACACACACCTGTTGCAACCTGTTTCCCTTACATTCACAT 1058  
Db 905 TTTTCCATGACCTTATACACACACCTGATGATTCATCTTGTATCTTACATTCACACT 964  
Qy 1059 ATCATGCAAGAGGACCAAGGACCTCAAGCCATCAAGCCATCTTGGTGTATACAGGATTCG 1118  
Db 965 ATCATGCAAGAGGACCAAGGATGCAATCAACCCAGTCTTGGGTGATTTATTAAGATTG 1024  
Qy 1119 ACAGGACTCCATTTTCAAGCAATGTGAGAGGACCAAGGATGCAATTTACATTCGAGC 1178  
Db 1025 ATAGGACTCTTATTTCAAGCAATGTGAGAGGACCAAGGATGCAATTTATTAAGATTG 1084  
Qy 1179 AAGATGCAAGAGGACCAAGGACATATTTGTTACCAATAAATGTAA 1228  
Db 1085 CAGATGAAGATACTGAACACAAAGGTTTACTGGTACCAATAAATGTAA 1134

## RESULT 8

US-10-772-227-6

[illegible]

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Db 17 ATGTCGAACATCGAATAAATCGGTCAATGGAACGTGCTCGGTTGATCCAGTACCTTCT 76
Qy 168 CGTTAAGTGATCTAAGAAAGCAATCCCTGACATTTGCTTCGGCGATCCGCGGTCTGGT 227
Db 77 CGCTAAGTGATTTAAGCAAGCAATCCCTCCCAATGCTTCAGCGATCTGTCATCCCGTT 136
Qy 228 CATCTGCTAGGTAGTTCAGGATCTCATATACACCTTCCTTTTATACAGGTCGCGACA 287
Db 137 CATCTTACTATGTAGTTACAGATCTCATATATGCGCTACATCTTCTTACTTCCTGCGGATA 196
Qy 288 CCTACATTCCTCACCTCCCTCCTCTCTAGTTTACTTAGCATGGCGGTTTACTGGTTTT 347
Db 197 AATATATTCGGAATCTCCTGCTCTCTAGCTACTTAGCTTGGCCCTTTACTGGTTCT 256
Qy 348 GCCAATCTTGATCCTCACTGGTTTATGGGTCCTCGGCCATGAATGCGGCCCATATGCGT 407
Db 257 GTCAAAGCTAGCATCCTCACTGGTTTATGGATCTCTCGGTCAATGAATGCGGTCAACATGCT 316
Qy 408 TTAGTGAGTACAGTGGATGTATAGCGCGGTTGGATTCGTCTCCATTCGGCTCTCCCTCA 467
Db 317 TTAGCGAGTACCAATGGGTTGACGACACTGTGGGCTTCATGGTCCACTCATTTCTCTCTCA 376
Qy 468 CCCCTTACTTTTCTTGGAAATACAGCCATCGAAAGCAATCGCAAAACAAATTCACCTCG 527
Db 377 CCCCGTATTTCTGTGGAAATACAGTACCGGATCACCATGCGCAACAGATTCATCG 436
Qy 528 AAAACGAGGAATTTACATTTCTCTAGAACTCACTGCTCCAGCTCAGGACTTACTCCACATAG 587
Db 437 ATAACGATGAAGTTTACATTTCCGAAAGCAAGTCCAAACTCGCGCTT-----ACCTATA 490
Qy 588 AATTTCTTGACAAACGCTGGTCCAACTCCTCATCTTGGTCAATCATGTTTAACTTAGGAT 647
Db 491 AACTTTCTTAAACACCGCTGGTCCGACTGTGTAGTTATGGTTATCATGTTTCAACCTTAGGAT 550
Qy 648 TTCCCTTTATACCTTTTACGAATGTTTTCAGGCAAGTACGATAGATAGATTACCAACCACT 707
Db 551 TTCCCTTTATACCTTTTGCAAAATATTTTCGGCAAGAGTACGACAGGTTTGGCAACCACT 610
Qy 708 TTGATCCATTTGAGCCGATCTTTCACCGAGCGGTGAGCGAATCCAGGTTCGGTTTATCAGATC 767
Db 611 TCGACCCCATGAGTCCAAATTTTCAAGGAAGGTGAGCGGTTTCAGGCTCTTTCGGATC 670
Qy 768 TTGGTATCGTTCAGTGTGTTTACGAGTCAAGTTTCTTGTGTACAAACAAAGATTTGGTT 827
Db 671 TTGGGCTTCTTGTCTGTGTTTATGGAATTTAAAGTTGCTGTAGCAAGAAAGAGCTGGT 730
Qy 828 GGGTGATGTGATGTATGGAGTTCCAGTGATAGGCTTGAATTCCTTCATATCGTAATCA 887
Db 731 GGGTGGGTGTATGTATGGAGTTCCGATGCTAGGCGGTATTTAACCCCTTTTCGATATCATCA 790
Qy 888 CTTATCTGCACACACATCTGTGCTCACCCCATTTACGATTTCAACCGAATGGAATCGA 947
Db 791 CGTACTTGACACACACCCCATCAGTCTCTCTCTCATTTATGACTCAACTGAATGGAATCGA 850
Qy 948 TCAAGAGGCGCTTGACCAACATCGACAGAGATTTCCGTCCTCGAATCCGGTTTTCACG 1007
Db 851 TCAGAGGGGCGTGTGAGCAATCGATAGGAGCTTTGGGTTCATGAAATAGTGTTCCTCATG 910
Qy 1008 AGTTTACACACACACCCAGGTTGGACCACTTGTGTTTCCCTTACATTCACATTTATCATGAA 1067
Db 911 ATGTTTACACACACTCAGCTCATGATCATATGTTTTCATACATTTCCACACTATCATGGA 970
Qy 1068 AGGAGGCAAGCGAGCCATCAAGCCAACTCTGGGTGATTTACAGGATGATTCGACAGACTTC 1127
Db 971 AAGAGCAAGGGATGCAATCAATACTATAGGCGACTATTATATATGATGATGATAGGACTC 1030
Qy 1128 CATTTTTCAGCAATGTGGAGAGGCGCAAGGATGCAATTTTACATTCGAGCAAGATGAG 1187
Db 1031 CAATTTTGAAGACACTGTGGAGAGGCGCAAGGATGCAATGATGATGATGATGATGATGATG 1084
Qy 1188 ACAGCAAGCAAAAGGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1228
Db 368 GTGGGCTTTCATCATCCATTCATTTCTCTCCACCCCGTATTTCTCTTGGAAATACAGTCA 427
Qy 497 CGAAAGCCATGCAACAAATTTCACTCGAAACAGGAAAGTTTACATTTCTTAGAACT 556
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## RESULT 10

US-09-981-124-3

; Sequence 3, Application US/09981124

; Patent No. US20020166144A1

; GENERAL INFORMATION:

; APPLICANT: Green, Allan

; APPLICANT: Singh, Surinder

; APPLICANT: Lenman, Marit

; APPLICANT: Stymne, Sten

; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD

; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD

; FILE REFERENCE: 26-98A

; CURRENT APPLICATION NUMBER: US/09/981,124

; CURRENT FILING DATE: 2001-10-17

; PRIOR APPLICATION NUMBER: US 09/059769

; PRIOR FILING DATE: 1998-04-14

; PRIOR APPLICATION NUMBER: US 60/043706

; PRIOR FILING DATE: 1997-04-16

; PRIOR APPLICATION NUMBER: AU P06223

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: AU P06226

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: US 60/050403

; PRIOR FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1309

; TYPE: DNA

; ORGANISM: Crepis sp.

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (937)..(937)

; OTHER INFORMATION: N is any nucleotide residue

; NAME/KEY: CDS

; LOCATION: (26)..(1147)

; OTHER INFORMATION:

; NAME/KEY: misc feature

; LOCATION: (901)..(901)

; OTHER INFORMATION: N is any nucleotide residue

US-09-981-124-3

Query Match 46.8%; Score 657.6; DB 3; Length 1309;

Best Local Similarity 76.4%; Pred. No. 1.8e-169;

Matches 836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

Qy 137 GAACGAGCCCGGATTTGATCCGCGCATTTCTCGTTAAGTGATCTAAAGAAAGCAATCCCT 196

Db 68 GAACGTGTCTCAGTTGATCCAGTAACTTCTCAGTGATGTTGAGCAAGCAATCCCT 127

Qy 197 GCACATTCCTTCCGCGGATCCGCGTCTGTCATCTCTCTAGTGTTCAGGATCTCAT 256

Db 128 CCACATTCCTTCCAGCGATCTGTCATCGTTTCATCTTATAGTGTTCAGGATCTCATA 187

Qy 257 ATACCTTCCTTTTATACACCGTCCCAACACCTACATTCCTCACCTCCCTCTCTCTA 316

Db 188 ATTGCTACATCTTCTACTTCTCTTCCCAACACATATATCCCTAATCTCCCTCATCTCTA 247

Qy 317 GTTTACTTTAGCATGCGCGTTTACTGTTTGGCAATCTTGCATCTCTCACTGGTTTATGG 376

Db 248 GCCTACTTAGCTTGGCCGCTTTACTGGTTCTGTCAAGTAGGCTCTCACTGGGTTATGG 307

Qy 377 GTCTCTCGGCCATGAATGCGGCCATCATGCTTTAGTAGTACCACTGAGTGGATGATTAACGCC 436

Db 308 ATCTCTCGGCCATGAATGTTGGTCAACCATGCTTATATGCAACATACATGGGTTGACGAC 367

Qy 437 GTTGATTCGTCCTCCATTCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 496

Db 368 GTGGGCTTTCATCATCCATTCATTTCTCTCTCCACCCCGTATTTCTCTTCTTCTTCTTCT 427

Qy 497 CGAAAGCCATGCAACAAATTTCACTCGAAACAGGAAAGTTTACATTTCTTAGAACT 556

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Db 428 CGGAATCACCATTCCAAACAAGTTCGATTGATAAGCATGAAGTTACATTCGAAAAAGC 487
Qy 557 CAGTCCAGCTCAGGACTTACTCCATACAGAAATTTCTTGACAAACAGCTGTCGAATC 616
Db 488 AAGTCNAACCAAGGT-----ATCTATAAATCTTTHAACAAACCCACCTGTCGACTG 541
Qy 617 CTCATCTTGCTCATCATGTTAACTTAGGATTTCTTTATACCTCTTAAACGAATGTTTCA 676
Db 542 TTGGTTTTGGTTATCATGTTTCACTTAGGATTTCTTTATACCTCTTGAACAAATTTTCC 601
Qy 677 GGAAGAAGTACATAGATTACCAACCACTTTGATCCATTGAGCCGATCTTACCGAG 736
Db 602 GGAAGAANAATACATAGTTTGGCAACCACTTCCAGCCCAATGATGATGATTTTCAAGAA 661
Qy 737 CGTGAGCGAATCAGGTTGGTTATCAGATCTTGGTATCGTTCAGTGTGTTTACGAGCTC 796
Db 662 CGTGAGCGGTTTCAGTCTCTTTCGATCTTGGTCTTCTGCTGTTGTTTATGGAAT 721
Qy 797 AAGTTTCTTGTACAAACAAAGGATTTGGTTGGGTGATGTCATGATGAGTTTCCAGTG 856
Db 722 AAAGTTGCTGTAGCAAAATAAGAGCTGCTTGGGTGGCGTGCATGATGAGTTCCGGTG 781
Qy 857 ATAGGTCTGAAATTCCTTATATATCGTAATCATCTTATCTGCACACACACATCTGTCTCA 916
Db 782 CTAGGCGTATTTACCTTTTTCGATGTGATCACGCTTCTTACACACACCACTCATGCTGCG 841
Qy 917 CCCCATTACGATTCACCGAATCGAATCGAATCGAATCGAATCGAATCGAATCGAATCGAAT 976
Db 842 CCTCATATGATTAACATGAATGGAATCGAATCGAATCGAATCGAATCGAATCGAATCGAAT 901
Qy 977 GATTTCCGCTCTCTGAATCGGTTTTTCCAGAGCTTACACACACCAACCGTTGTCACCAT 1036
Db 902 GACTTTGGGTTCTGATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 961
Qy 1037 TTGTTTCCCTACATTCACATTAATCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1096
Db 962 TTGTTTTCATACATTCACACTATCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1021
Qy 1097 TTGGGTGATTTACAGGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1156
Db 1022 TTGGGCGACTTTTATATGATCGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1081
Qy 1157 AAGGAATGCAATTTACATTCGAGCAAGATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1216
Db 1082 AGGAATGCAATGATACATCGAGC-----CTGATAGCAAGCTCAAAGGTGTTTATGGTAT 1135
Qy 1217 CATAAATGTAATC 1230
Db 1136 CATAAATGTAATC 1149
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## RESULT 11

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US-10-772-227-12
; Sequence 12, Application US/1077227
; Publication No. US20040168213A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Williams, Deryck J.
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLeod, Merry B.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; FILE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772, 227
; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; PRIOR FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 12
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Crepis biennis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1140)
; US-10-772-227-12
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Query Match 45.9%; Score 646; DB 8; Length 1143;
Best Local Similarity 73.8%; Pred. No. 2.6e-166;
Matches 852; Conservative 0; Mismatches 290; Indels 12; Gaps 2;
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Qy 75 TGGGAAGGTAGCAGAATGTCCGATTCATATGATGATCGAATGAAAGATCATGATATGG 134
Db 2 TGGGTGAGGTGGAAGATGCGGTTCTTCTTCAAGAAATCGAAGAACCGACACCA 61
Qy 135 ACGAAGCGCCGATTCGATTCGCGGCCATTCCTGTTAGTGTCTTAAGAAAGCAATCC 194
Db 62 CAAAGCGTGTGCGGTGCGAGAAACCGCCCTTTCTCGGTGGAGATCTGAAGAAAGCAATCC 121
Qy 195 CTGCATTTGCTTCCGCGCATCGCGCTGCTGCTCATCTCTGCTAGTAGTTTCAGATCTCA 254
Db 122 CTTCCCATTTGCTTCCGCGCATCTGTAATCGTTTCTTACTATGATGATTCAGATCTCA 181
Qy 255 TTATCACTTCTCTTTTATACAGGTGCGCAACACCTTACATTCCTCACTCCCTCTCTC 314
Db 182 TTATGCTTACATCTTCTTCTTCTTCCGTAATAATATATTCGATTTCTCCCTGCTCTC 241
Qy 315 TAGTTTACTTAGATGCGCGGTTTACTGTTTGGCAATCTTGCAATCTTGCAATCTCTGTTAT 374
Db 242 TAGCTTACTTAGTGTGCGGCTTTACTGTTTCTGTCAGCTAGCATCTCTCTGTTAT 301
Qy 375 GGGTCTCGCGCATGAATCGGCGCATCATGCTTCTGATGAGTACAGTGGATGATAACG 434
Db 302 GGATCTCTCGGTATGAATGCGGTACCATGCTTTAGCGAGACCAATGGTTGAGCACA 361
Qy 435 CGGTTGGAATTCCTTCCATTCGGCTCTCTCTCACCCCTTACTTTTCTTGGAAATACAGCC 494
Db 362 CTGTGGCTTCTCATGTTCCACTCATTTCTCTCACCCGTTATTTCTCGTGGAAATACAGTC 421
Qy 495 ATCGAAGCACCATGCAAAACACAAATTCATCTCGAAGAGGAGGATTTTACATTTCTAGAA 554
Db 422 ACCGAATCACCATGCAAAACACAAATTCATTAACGATGAAGTTTACATTTCCGAAA 481
Qy 555 CTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTGACACACAGCTGTCGAA 614
Db 482 GCAAGTCCAAACTCGCGCTT-----ACCTATAAATCTTAAACACCCGCTGGTCGAC 535
Qy 615 TCCTCATCTTGGTCAATCATGTTAACTTAGGATTTCTTTTATACCTTCTTAAACGAATGTT 674
Db 536 TGTAGTTATGTTATCATGTTTCACTTAGGATTTCTTTTATACCTTCTTGAACAAATATT 595
Qy 675 CAGGCAAGAGTACGATAGATTACCAACCATTTGATCAATGAGCCGATCTTCAACCG 734
Db 596 CCGGCAAGAGTACGACAGGTTTGCACACACTTCGACCCCATGAGTCCAAATTTTCAAG 655
Qy 735 AGGTCAGCGAATCAGGTTGCGTTATCAGATCTTGGTATCGTTGAGTGTGTTTACGGAC 794
Db 656 AAGCTGAGCGGTTTCAAGGTTCTGCTTTTGGATCTTGGGCTTCTTGTGTTTATGGAA 715
Qy 795 TCAAGTTTCTGTACAAACAAAGGATTTGGTTGGGTGATGTCATGTATGAGTTCAG 854
Db 716 TTAAGTTCTGTAGCAAGAAAGAGCTGCGTGGGTGGGTGATGATGATGAGTTCGA 775
Qy 855 TGATAGTCTGAATTTCTTCTTATATGTAATCATCTTATCTGACACCAACACATCTCTG 914
Db 776 TGCTAGCGGTATTTACCTTTTCGATATCATCAGTACTTTCACACACACCCATCAGTCG 835
Qy 915 CACCCCATTTACGATTCAGAACTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 974
Db 836 CTCCTCATTTAGCTCACTCACTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 895
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QY 975 GAGATTTCGGTCTCTGTAATCGGGTTTCCAGGAGTTTACACACCCACGTTGTGCACC 1034
D 986 GGGACTTTGGGTTCAATGATAGTGTTCATGATGTTTACACACACTCACGTCATGCATC 955
QY 1035 ATTTGTTTCCCTACATTTCCACATTTATCATGCAAGAGGCGCAAGCGAGCCATCAAGCCAA 1094
D 956 ATATGTTTTCATACATTTCCACATCATCATGCAAGAGGCGCAAGGATGCATCAATCAATACA 1015
QY 1095 TCTTGGGTGATTTACAGGATGATCGACAGGATCTCCATTTTCAAAGCAATGTGGAGAGG 1154
D 1016 TCATAGGCGACTATTATATGATCGATAGGACTCCAAATTTTGAAGCACTGTGGAGAGG 1075
QY 1155 CAAAGGAATGATTTACATTCAGGAGGATGCAAGAGGCGCAAGGATGCATCAATCAATCA 1214
D 1076 CCAAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129
QY 1215 ACCATAAAATGTAA 1228
D 1130 ATCATAAATGTGA 1143

RESULT 12
US-10-912-534-12
; Sequence 12, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbeke, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; TITLE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Crepis biennis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1140)
US-10-912-534-12

Query Match 45.9%; Score 646; DB 10; Length 1143;
Best Local Similarity 73.8%; Pred No. 2,6e-166;
Matches 852; Conservative 0; Mismatches 290; Indels 12; Gaps 2;

QY 75 TGGGAGAGGTAGCAGAAATGTCGGATTCATATGATGATCGAATGAAAGATCATGATAGG 134
D 2 TGGGTGCGAGTGGAGAAATGCCGTTCTTCTTCCAAAGAAATCGGAACCGACACCA 61
QY 135 ACGAAGAGCCCGGATTTGATCGGGCGCATTTCTGTTAAGTATCTTAAGAAAGCAATCC 194
D 62 CAAAGCGTGTGCGCGGAGAAACCGCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCC 121
QY 195 CTGCAATTTCTCGGGCATCGCGTCTGTGTCCTGTCCTGTCAGTGTTCAGGATCTCA 254
D 122 CTCCCATTTGCTTCAGCGCATCTGAATCCGTTCTTCTTACTTGTAGTTTACGATCTCA 181
QY 255 TTATCACCTTCTTTTATACAGGTCGCAACACCTTACATTCCTCACCTCCCTCCCTC 314
D 182 TTATTGCTTACATCTTCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 241
QY 315 TAGTTTACTTAGCATGCGCGGTTTACTGGTTTGTGCAATCTTGCATCCTCACTGGTTTAT 374
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Db 242 TAGCTACTTAGCTTGGCCCTTTACTGGTTCTGCTCAAGCTAGCATCTCTCACTGGTTAT 301
QY 375 GGGTCTCGGCATGAATGCGGCCCATCATGCTTTTAGTGAAGTCAAGTGGATGATAAG 434
D 302 GGATCTCGGTTCATGAATGCGGTTCACATGCTTTTAGCGAGCAATATGGGTTCAGCACA 361
QY 435 CCGTTGATTTGCTCTCATTTGCGGTCTCTCACCCCTTACTTTCTTTGGAATACAGCC 494
D 362 CTGTTGGGCTTCATGGTCCACTCATTTCTCTCTCACCCGATTTCTCTGTTGGAATACAGTC 421
QY 495 ATCGAAGACACATGCAAAACAAATTCACATTCGAAACGAGGAAGTTTACATTTCTAGAA 554
D 422 ACCGGAATCACCATGCCAACAAAGTTCCATTTGATAGAGTGAAGTTTACATTTCCGAAA 481
QY 555 CTCAGTCCCAGCTCAGGACTTACTCCACATACGAATTTTGTGAACAACAGCGCTGTGCA 614
D 482 GCAAGTCCAAACTCGCGCTT-----ACCTATAAATCTTTAAACAACCCGCTGTGTCGAC 535
QY 615 TCCTCATCTTGGTTCATCATGTTTAACTTAGGATTTCTTTTATACCTCTTAAGATGTTT 674
D 536 TGTTAGTTATGTTTATCATGTTTCACTCCCTAGGATTTCTCTTTATACCTCTTGACAAATAT 595
QY 675 CAGCAAGAAGTACGATAGATTTTACCAACCACTTTTGATCCATTTGAGCCCGATCTTCAACG 734
D 596 CCGCAAGAGTACGACAGGTTTGGCAACCACTTCGACCCCATGAGTCCAATTTTCAAG 655
QY 735 AGCGTAGCGAATCAGGTTGCGTTTATCAGATCTTTGGTATCGTTGCGAGTGTTCAGGAC 794
D 656 AACGTGAGCGGTTTTCAGGTCTTGGTTCGGATCTTGGCTTCTTGGCTGTGTTTATGAA 715
QY 795 TCAAGTTTCTGTACAAACAAAGATTTGTTGGTGTGATGTCATGTCATGTCAGTTCCAG 854
D 716 TTAAGTTGCTGTAGCAAGAAAGAGGCTGCGTGGTGGCGTGTATGTATGAGTTCCGA 775
QY 855 TGATAGGTCTGAATTTCTTCAATTTATCGTAATCACTTATCTGCACACACACATCTGCTGT 914
D 776 TGCTAGGCGTATTTACCTTTTCGATATCATCATGCTACTTGCACACACACCCATCACTGT 835
QY 915 CACCCCATTTACGATTTCAACCAAGTGAATCGATCAAGAGGCGTTGACCAATTCGACA 974
D 836 CTCCTCATTTATGACTCAACTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 895
QY 975 GAGATTTGCGTCTCTGTAATCGGGTTTTCACAGCGTTTACACACCCACCGTTGTCACC 1034
D 896 GGGACTTTTGGGTTCAATGAATAGTGTTCATGATGATGATGATGATGATGATGATGATGAT 955
QY 1035 ATTTGTTTCCCTACATTTCCACATTTATCATGCAAGAGGCGCAAGCGAGCCATCAAGCCAA 1094
D 956 ATATGTTTTCATACATTTCCACATCATCATGCAAGAGGCGCAAGGATGCAATCAATACA 1015
QY 1095 TCTTGGGTGATTTACAGGATGATCGACAGGATCTCCATTTTCAAAGCAATGTGGAGAGG 1154
D 1016 TCATAGGCGACTATTATATGATCGATAGGACTCCAAATTTTGAAGCACTGTGGAGAGG 1075
QY 1155 CAAAGGAATGATTTTACATCGGAGCAAGATGCAAGCAAGCAAGCAAGCAAGCAAGCAAT 1214
D 1076 CCAAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129
QY 1215 ACCATAAAATGTAA 1228
D 1130 ATCATAAATGTGA 1143

RESULT 13
US-10-622-774-10
; Sequence 10, Application US/10622774
; Publication No. US20050022270A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Hildebrand, David
; APPLICANT: Hatanaka, Tomoko
; TITLE OF INVENTION: RECOMBINANT STOKESIA BPOSYGENASE GENE
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FILE REFERENCE: 050229-0377  
CURRENT APPLICATION NUMBER: US/10/622,774  
CURRENT FILING DATE: 2003-07-21  
PRIOR APPLICATION NUMBER: 60/396,406  
PRIOR FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 10  
LENGTH: 1344  
TYPE: DNA  
ORGANISM: Crepis palaestina  
US-10-622-774-10

Query Match 45.5%; Score 640.4; DB 9; Length 1344;  
Best Local Similarity 75.5%; Pred. No. 9.9e-165;  
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 137 GAACGAGCCCCGATTCGATCCGGCGCCATCTCGTTAAGTGATCTAAAGAAAGCAATCCCT 196  
DB 75 GAACGAGTCTCAGTTGATCCAGTAACCTTCTCACTGAGTGAATGAAGCAAGCAATCCCT 134

QY 197 GCACATTGCTCCGGGATCCCGGCTCGTCTGATCTGCTAGCTAGTTCAGGATCTCAT 256  
DB 135 CCCATTGCTTCAGAGATCTGTAATCCGCTCACTACTATGTTGTTCAAGATCTCAT 194

QY 257 ATCACCTTCCTTTTATACAGGTCGCCAACACCTACATTCCTCACCTCCCTCTCTCTA 316  
DB 195 ATTGCTACATCTTCTACTTCTTCCGCAACACATATATCCCTACTCTTCTACTAGTCTA 254

QY 317 GTTTACTAGCATGGCGGTTTACTGGTTTGGCAATCTTGCACTCTCACTCTGTTTATGG 376  
DB 255 GCGTACTAGCTTGGCGGTTTACTGGTTTCTGTCAAGCTAGGCTCTCACTGGCTTATGG 314

QY 377 GTCTCGGCCCAAGTCCGCCCATCATGCTTTAGTGAGTACCAGTGAATGATACGCC 436  
DB 315 ATCTCGGCCCAAGTGTGTACCAGTCTTTAGCACTACACATGGTTTGACGACAT 374

QY 437 GTTGAATTCGTCTCCATTCGGCTCTCTCCACCCCTTACTTTCTTGGAAATACAGCCAT 496  
DB 375 GTGGGCTTCACTCTCACTCATTTCTCTCCACCCGCTATTTCTTGGAAATTCAGTCA 434

QY 497 CGAAGCACATGCAAAACAAATTCATCTGAAACAGAGAGTGTATTCATCTTAGAAT 556  
DB 435 CGGAATCACCATTCCAACACAAAGTTCGATGATAACGATGAAGTTTACATTCGAAAGC 494

QY 557 CAGTCCGCTCAGGACTTACTCCATACGATTTCTTGACAAACGCGCTGTGCAATC 616  
DB 495 AAGTCCAAACTCGCGCT-----ATCTATAAACTTCTTAACAAACCCACTGTGCGCTG 548

QY 617 CTCATCTTGTGATCATGTGTTAAGTTTAGGATTTCTTTATACCTCTTAACGAATGTTCA 676  
DB 549 TTGGTTTGTATCATGTTCACCTTAGATTTCTTTATACCTCTTGACAAATATTTCC 608

QY 677 GCGAAGATGATAGATTACCAACCACTTTGATCCATTTAGCCGATCTTACCGAG 736  
DB 609 GCGAAGAAATACGACAGGTTTGCAACCACTTCGACCCCATGAGTCCAATTTTCAAGAA 668

QY 737 CGTGAGGAAATCCAGGTTGGTTATCAGATCTTGGTATCGTTGCAGTGTTCAGGACT 796  
DB 669 CGTGAGCGGTTTTCAGGTTCTTCTTTCGATCTTGGTCTTCTTGGCGGTGTTTATGAA 728

QY 797 AAGTTTCTTGTACAAACAAAGATTTGGTTGGTGATGTGATGTGAGTTCAGGTG 856  
DB 729 AAGTTTCTGTAGCAATTAAGAGAGCTGTTGGGTAGCGTGATGTGAGGTTCGGTA 788

QY 857 ATAGGCTGTAATTCCTTCAATTAATCGTAATCACTTATCTGCACACACATCTGCTCA 916  
DB 789 TTAGGCGTATTACCTTTTTCGATGTGATCACCTTCTTGCACCAACCCATCAGTCTG 848

QY 917 CCCATTAGATTCACCGGAATGGAATCGAATCAAGAGGACCTTGACCAACATCGACAGA 976  
DB 849 CCTCATTTATGATTCAGTGAATGGAATCGATCAGAGGGGCGCTTGTGAGCAATCGATAG 908

QY 977 GATTTGGTCTCCTGAAATCGGGTTTTTCCACGAGCTTACACACACCCAGTGTGTCACCAT 1036  
DB 909 GACTTTGGATTCCTGAATAGTGTGTTTCCATGATGTTTACACACACTCATGTCATGATCAT 968

QY 1037 TTGTTTCCCTACATTCACATTCATGCAAGAGGAGGCAAGCGAGGCCATCAAGCCAATC 1096  
DB 969 TTGTTTTCATACATTCACACTATCATGCAAGAGGAGGCAAGGATGCAATCAAGCCAATC 1028

QY 1097 TTGGGTGATTCAGGATGATCGACAGGATCTCATTTTCAAAGCAATGTGGAGAGAGGCC 1156  
DB 1029 TTGGGCGACTTTTATATGATCGACAGGATCTCAATTTTAAAGCAATGTGGAGAGAGGCC 1088

QY 1157 AAGGAATGATTTATACATCGAGCAAGATCGACAGCAACACAAAGGGACATATGTTATC 1216  
DB 1089 AGGGAGTGTGATGATACATCGAGC-----CTGATAGCAAGCTCAAAGGTGTTTATTGGTAT 1142

QY 1217 CATAAATGTAATC 1230  
DB 1143 CATAAATGTGATC 1156

RESULT 14  
US-09-981-124-1  
; Sequence 1, Application US/09981124  
; Patent No. US20020166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Marit  
; APPLICANT: Stymme, Sten  
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MODI  
; FILE REFERENCE: 26-98A  
; CURRENT APPLICATION NUMBER: US/09/981,124  
; CURRENT FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: US 09/059769  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/043706  
; PRIOR FILING DATE: 1997-04-16  
; PRIOR APPLICATION NUMBER: AU P06223  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR APPLICATION NUMBER: AU P06226  
; PRIOR APPLICATION NUMBER: US 60/050403  
; PRIOR FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1358  
; TYPE: DNA  
; ORGANISM: Crepis palaestina  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1151)  
; OTHER INFORMATION:  
US-09-981-124-1

Query Match 45.5%; Score 640.4; DB 3; Length 1358;  
Best Local Similarity 75.5%; Pred. No. 1e-164;  
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 137 GAACGAGCCCCGATTCGATCCGGCGCCATTCCTCGTTAAGTGATCTAAAGAAAGCAATCCCT 196  
DB 75 GAACGAGTCTCAGTTGATCCAGTAACCTTCTCACTGAGTGAATGAAGCAAGCAATCCCT 134

QY 197 GCACATTGCTCCGGGATCCCGGCTCGTCTGATCTCTGCTAGTGTAGTTCAGGATCTCAT 256  
DB 135 CCCATTGCTTCAGAGATCTGTAATCCGCTCACTACTATGTTGTTCAAGATCTCAT 194

QY 257 ATCACCTTCCTTTTATACAGGTCGCCAACACCTACATTCCTCACCTCCCTCTCTCTA 316  
DB 195 ATTGCTACATCTTCTACTTCTTCCGCAACATATATCCCTACTCTTCTCTACTAGTCTA 254



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QY 317 GTTACTTAGCATGGCCGGTTTACTGGTTTGGCAATCTTGCACTCCTCACTGGTTATGG 376
Db 255 GCCTACTTAGCTGGCCGGTTTACTGGTTCTGTCAAGCTAGCGTCTCACTGGCTTAGG 314
QY 377 GTCCTCGGCCAATGAATGGGCCATCATGCCCTTAGTGTAGTACCACTAGTGAATGAAGCC 436
Db 315 ATCTCTGGCCAGAAATGTGGTCAACATGCCCTTAGCACTACATAGTTTGAACACT 374
QY 437 GTTGGATTGCTCTCCATTCGGCTCTCTCAACCCCTTACTTTTCTTGGAAATACAGCAAT 496
Db 375 GTGGCTTTCATCTCCACTCATTTCTCTCTCAACCCCGTATTTCTCTTGGAAATTCAGTCA 434
QY 497 CGAAGCAACATGCAACACACAAATTCATCGAAGAGGAGGAGTTTACATTTCTTAGACT 556
Db 435 CGGAATCACCAATCCACACACAAATTCGATTCGATTAACGATGAAGTTTACATTTCCGAAAGC 494
QY 557 CAGTCCCAAGCTCAGGACTTACTCACATACGAATTTCTTGACACACGCGCTGGTCAATC 616
Db 495 AAGTCCAAACTCGCGCT-----ATCTATAAATCTTCTTAACACCCACCTGGTGGCTG 548
QY 617 CTCATCTTGGTCATCATGTTAACTTAGGATTTCTTTATACCTCTTAAACGAATGTTTCA 676
Db 549 TTGGTTTTGATTATCATGTTCAACCTAGGATTTCTTTATACCTCTTGACAAATATTTC 608
QY 677 GCGAAGAGTAGGATAGATTTACCAACCACTTGTATCCATTTGAGCCCGATCTTCAACGAG 736
Db 609 GCGAAGAAATACGACAGGTTTGCACCAACCACTTCGACCCCATGAGTCCAAATTTCAAGAA 668
QY 737 CGTGAGCAATCCAGTTGCGTTATCAGATCTTGTGATCGTTGCAAGTGTATTTAGCGACT 796
Db 669 CGTGAGCGGTTTCAAGTCTTCTTTCGATCTTGTCTTCTTGGCTGTTTATGGAAT 728
QY 797 AAGTTTCTTGACAAACAAAGGATTTGGTTGGGTGATGTGCATGTATGAGATTTCCAGTG 856
Db 729 AAGTTTCTTGACAAATAAGGAGCTGTTGGGTAGCGTGCATGTATGAGATTTCCGGA 788
QY 857 ATAGTCTGAATCTCTTCAATTCGTATACCTTATCTGACCAACACATCTGCTGCTCA 916
Db 789 TTAGCGGTATTTACCTTTTTCATGTGATCACCTTTCTTGCACCAACACCATCAGTCGTCG 848
QY 917 CCCCATACGATTCACCGAATGGAATCGGATCAAGGAGGCTTGACCAACATCGACAGA 976
Db 849 CCTCATATGATTTCACTGAATGGAATCTGATCAGAGGGGCTTGTGAGCAATCGATAGG 908
QY 977 GATTTGGTCTCTCGAATCGGGTTTTTCCACGAGTTTACACACACCCAGTGTGACCAAT 1036
Db 909 GACTTTGGATTCCTGAATAGTGTTTTCCATGATGTTTACACACACTCATGTATGCATCAT 968
QY 1037 TTGTTTCCCTACATTCACATATATCATGCAAGGAGGCAAGGAGGCTCATCAAGCCAATC 1096
Db 969 TTGTTTTCATACATTTCCACACTATCATGCAAGGAGGCAAGGAGTGCATCAAGCCAATC 1028
QY 1097 TTGGGTGATTCAGGATGATCGACAGGACTCCATTTTCAAGCAATGTGGAGAGGCCC 1156
Db 1029 TTGGCGAGCTTTTATGATCGACAGGACTCCATTTTAAAGCAATGTGGAGAGGGC 1088
QY 1157 AAGGAATGCATTTATCATCGAGCAAGATGACAGACAGCAAGCAATATTTGGTATC 1216
Db 1089 AGGAGTGCATGTACATCGAGC-----CTGATGCAAGCTCAAAGGTGTTTATTTGGTAT 1142
QY 1217 CATAAATGTATTC 1230
Db 1143 CATAAATTTGTGATC 1156
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## RESULT 15

US-10-772-227-32

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/ Sequence 32, Application US/1077227
/ Publication No. US20040168213A1
/ GENERAL INFORMATION:
/ APPLICANT: Verbsky, Michelle L.
/ APPLICANT: Baubliche, Catherine
/ APPLICANT: Williams, Deryck J.
```

```
/ APPLICANT: Kloek, Andrew P.
/ APPLICANT: Davila-Aponte, Jennifer A.
/ APPLICANT: Hresko, Michelle Coutu
/ APPLICANT: McLaaird, Merry B.
/ TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
/ TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
/ FILE REFERENCE: 12557-016001
/ CURRENT APPLICATION NUMBER: US/10/772,227
/ PRIOR FILING DATE: 2004-02-04
/ PRIOR APPLICATION NUMBER: US 60/445,293
/ PRIOR FILING DATE: 2003-02-05
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 1125
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: hypothetical sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1122)
US-10-772-227-32
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Query Match 45 43; Score 638.6; DB 8; Length 1125;
Best Local Similarity 74.5%; Pred. No. 2.8e-164;
Matches 835; Conservative 0; Mismatches 274; Indels 12; Gaps 2;

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Db 17 ATAGTCGAACATCTAAGAAGTCTGTCATGGAACGTGCTCTGTTGATCCAGTACCCCTTCT 76
QY 168 GGTAAAGTATCTAAAGAAAGCAATCCCTGCAATGCTTCGGGGGATCCCGCTCTGGT 227
Db 77 CTCCTAAGTATTTGAAGCAAGCAATCCCTCCCAATGCTTCCACGAGATCTGTATCCGTT 136
QY 228 CATCTCTAGTATGATTCAGGATCTCATTTATACCTTCTCTTTTATACAGGTTCGCAACA 287
Db 137 CATCTTACTATGTAGTTTACAGATCTCATTTATGCTCATCATCTTCTCTCTTCCGCGACA 196
QY 288 CCTACATTTCTCACTCCCTCTCTCTAGTTTACTTAGCATGCGCGTTTACTGGTTTT 347
Db 197 AATACATTTCCAAATTTCTCCCTGCTCTCTAGCTTACTTAGCTTGGCCCTTTACTGGTTCT 256
QY 348 GCCAATCTTGATCTCTCACTGGTTTATGGTCTCTCGGCATGAAATGGGCCATCATGCT 407
Db 257 GTCAAGCTAGCATCTCTCACTGGTTTATGGATCTCTCGGTATGAATGCGGTCAACATGCT 316
QY 408 TTAGTGAGTACCAAGTGGATTCGATTAACGCGGTTGGATTTGCTCTCCATTTCCGCTCTCTCA 467
Db 317 TTAGCGAGTACCAATGGGTTTACGACACTGTGGGCTTCTATGTTCACTCATTTCTTCTCA 376
QY 468 CCCCTTACTTTTCTTGGAAATACAGCCATTCGAAAGCACCATGCAAAAGCACCAAAATTCAC 527
Db 377 CTCCTTACTTCTTGGAAATACAGTCAAGAAATCACCATGTCGCAACACAAAGTTCCATTG 436
QY 528 AAAACGAGGAAGTTTACATCTTAGAATCTAGTCCAGCTCAGGATCTTCTCCACATAGC 587
Db 437 ATAAAGTAAAGTTTATCATTTCTTAAGAGCAAGTCCAAACTCGCTCTT-----ACCTATA 490
QY 588 AATTTCTTGACACACGCGCTGTCGAATCTCTGTCATCTTGGTTCATCATGTTAACTTAGGAT 647
Db 491 AGCTTCTTAAACACCTCCAGAAAGGCTGTAGTTATGTTTATCATGTTTCAACCTTAGGAT 550
QY 648 TTCCTTTTATACCTCTTAAAGAAATGTTTTCAGGCAAGAGTACGATAGATTTTACCAACCACT 707
Db 551 TTCCTTTTATACCTCTTGAACAAATATTTCCGCAAGAAAGTACGACAGGTTTGCACCAACT 610
QY 708 TTGATCCATTTGAGCCCGATCTTCCAGCGCTGAGCGGAATCCAGGTTGCGTTTATCAGATC 767
Db 611 TCGACCCCATGAGTCCCAATTTTCAAGGAACGCTGAGAGGTTTTCAGGCTTGTCTTCTGATC 670
QY 768 TTGGTATCGTTGCAAGTGTTTTACGAGACTCAAGTTTCTTGTACAAACAAAGGATTTGGTT 827
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model  
Run on: September 24, 2006, 23:05:00 ; Search time 294 Seconds  
(without alignments)  
8948.228 Million cell updates/sec

Title: US-10-622-774-1  
Perfect score: 1406  
Sequence: 1 gtaggtttgggtgcggtg.....aaaaaaaaaaaaaaaaaaaaa 1406

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq.\*  
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9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|----|-------------------|-------------------|
| 1          | 870   | 61.9        | 1364   | 2  | US-08-872-302-3   | Sequence 3, Appli |
| 2          | 657.6 | 46.8        | 1312   | 3  | US-09-059-769-3   | Sequence 3, Appli |
| 3          | 640.4 | 45.5        | 1358   | 3  | US-09-059-769-1   | Sequence 1, Appli |
| 4          | 611.2 | 43.5        | 1128   | 3  | US-09-161-994A-1  | Sequence 1, Appli |
| 5          | 426.2 | 30.3        | 1372   | 3  | US-09-133-962A-1  | Sequence 5, Appli |
| 6          | 426.2 | 30.3        | 1372   | 3  | US-09-763-331-5   | Sequence 1, Appli |
| 7          | 426.2 | 30.3        | 1372   | 3  | US-09-697-379-1   | Sequence 1, Appli |
| 8          | 426.2 | 30.3        | 1372   | 3  | US-10-116-212A-1  | Sequence 1, Appli |
| 9          | 424.6 | 30.2        | 2973   | 3  | US-09-133-962A-15 | Sequence 15, Appl |
| 10         | 424.6 | 30.2        | 2973   | 3  | US-09-697-379-15  | Sequence 15, Appl |
| 11         | 424.6 | 30.2        | 2973   | 3  | US-10-116-212A-15 | Sequence 15, Appl |
| 12         | 419.4 | 29.8        | 1422   | 4  | US-09-837-751-5   | Sequence 5, Appli |
| 13         | 417.2 | 29.7        | 1164   | 4  | US-10-185-578-1   | Sequence 1, Appli |
| 14         | 417.2 | 29.7        | 1222   | 2  | US-08-314-596-43  | Sequence 43, Appl |
| 15         | 417.2 | 29.7        | 1222   | 2  | US-08-320-982-43  | Sequence 43, Appl |
| 16         | 417.2 | 29.7        | 1222   | 2  | US-08-819-037-43  | Sequence 43, Appl |
| 17         | 417.2 | 29.7        | 1222   | 3  | US-08-819-037-43  | Sequence 43, Appl |
| 18         | 417.2 | 29.7        | 1448   | 2  | US-09-045-940-43  | Sequence 39, Appl |
| 19         | 417.2 | 29.7        | 1448   | 2  | US-08-314-596-39  | Sequence 39, Appl |
| 20         | 417.2 | 29.7        | 1448   | 2  | US-08-320-982-39  | Sequence 39, Appl |
| 21         | 417.2 | 29.7        | 1448   | 3  | US-08-819-037-39  | Sequence 39, Appl |
| 22         | 415.4 | 29.5        | 1476   | 2  | US-09-045-940-39  | Sequence 1, Appli |
| 23         | 412.4 | 29.3        | 1231   | 2  | US-08-872-302-1   | Sequence 44, Appl |

|    |       |      |      |   |                   |                   |
|----|-------|------|------|---|-------------------|-------------------|
| 24 | 412.4 | 29.3 | 1231 | 2 | US-08-320-982-44  | Sequence 44, Appl |
| 25 | 412.4 | 29.3 | 1231 | 3 | US-08-819-037-44  | Sequence 44, Appl |
| 26 | 412.4 | 29.3 | 1231 | 3 | US-09-045-940-44  | Sequence 44, Appl |
| 27 | 408   | 29.0 | 1155 | 2 | US-08-675-650B-1  | Sequence 1, Appli |
| 28 | 408   | 29.0 | 1426 | 3 | US-09-133-962A-3  | Sequence 3, Appli |
| 29 | 408   | 29.0 | 1426 | 3 | US-09-697-379-3   | Sequence 3, Appli |
| 30 | 408   | 29.0 | 1426 | 3 | US-10-116-212A-3  | Sequence 3, Appli |
| 31 | 407   | 28.9 | 1369 | 3 | US-09-133-962A-11 | Sequence 11, Appl |
| 32 | 407   | 28.9 | 1369 | 3 | US-09-697-379-11  | Sequence 11, Appl |
| 33 | 407   | 28.9 | 1369 | 3 | US-10-116-212A-11 | Sequence 11, Appl |
| 34 | 406.4 | 28.9 | 1155 | 3 | US-09-354-231B-13 | Sequence 13, Appl |
| 35 | 406.4 | 28.9 | 1155 | 3 | US-09-128-602B-13 | Sequence 13, Appl |
| 36 | 406.4 | 28.9 | 1155 | 3 | US-09-995-297-13  | Sequence 13, Appl |
| 37 | 406.4 | 28.9 | 1155 | 4 | US-09-771-904A-13 | Sequence 13, Appl |
| 38 | 405.2 | 28.8 | 1155 | 2 | US-08-675-650B-5  | Sequence 5, Appli |
| 39 | 404.8 | 28.8 | 1155 | 3 | US-09-354-231B-15 | Sequence 15, Appl |
| 40 | 404.8 | 28.8 | 1155 | 3 | US-09-354-231B-17 | Sequence 17, Appl |
| 41 | 404.8 | 28.8 | 1155 | 3 | US-09-128-602B-15 | Sequence 15, Appl |
| 42 | 404.8 | 28.8 | 1155 | 3 | US-09-128-602B-17 | Sequence 17, Appl |
| 43 | 404.8 | 28.8 | 1155 | 3 | US-09-995-297-15  | Sequence 15, Appl |
| 44 | 404.8 | 28.8 | 1155 | 3 | US-09-995-297-17  | Sequence 17, Appl |
| 45 | 404.8 | 28.8 | 1155 | 4 | US-09-771-904A-15 | Sequence 15, Appl |

ALIGNMENTS

RESULT 1  
US-08-872-302-3  
; Sequence 3, Application US/08872302  
; Patent No. 5846784  
; GENERAL INFORMATION:  
; APPLICANT: Hitz, William D  
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
; TITLE OF INVENTION: Developing Seeds of Vernonia galamensis  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. duPont de Nemours and Co.  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: USA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,302  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Majarian, William R  
; REGISTRATION NUMBER: P-41,173  
; REFERENCE/DOCKET NUMBER: BB-1084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-4926  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1364 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 103..1254  
US-08-872-302-3

Query Match 61.9%; Score 870; DB 2; Length 1364;  
Best Local Similarity 86.1%; Pred. No. 2.3e-229;

| Matches | 963; | Conservative   | 0;   | Mismatches | 155; | Indels | 0; | Gaps | 0; |
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| Qy      | 120  | AAGATCATGATATGACGAAACGAGCCCGATTTGATCCGGCGCCCATTTCTCGTTAAGTATC    | 179  |            |      |        |    |      |    |
| Db      | 149  | ATGATCATATATAAACGAAAGTGCACCGGTGTATCGGCACCATTTCTCGTTAAGCGATC      | 208  |            |      |        |    |      |    |
| Qy      | 180  | TAAAGAAAGCAATCCCTGCACATTTGCTTTCGGCGAATCGCGGTCTGTGTCATCTCTGCTACG  | 239  |            |      |        |    |      |    |
| Db      | 209  | TAAAGAAAGCAATCCCTCGCATTTGCTTTCAGCGATTCGCATCCGTTTCATCGTGTCTACG    | 268  |            |      |        |    |      |    |
| Qy      | 240  | TAGTTCAGGATCTCATTTATCACTTCCTTTTATACACGGTCGCGCAACACCTTACATCTCCTC  | 299  |            |      |        |    |      |    |
| Db      | 269  | TTGTTTCAGGATCTCATTTATTAACCTTCCTTTTATACACGCTCGCGCACTCTTACATCTCCTC | 328  |            |      |        |    |      |    |
| Qy      | 300  | ACCTCCCTCCTCCTTAGTTTACTTAGCATGCGCGGTTTACTGTGTTTTCGCAATCTTGCA     | 359  |            |      |        |    |      |    |
| Db      | 329  | TTCTTCTCCTCCTCTACTTACTTAGCATGCGCTGTGTTTACTGTGTTTTCGCAATCTTCGA    | 388  |            |      |        |    |      |    |
| Qy      | 360  | TCCTCACTGGTTTATGGGTCTCTCGGCCATGAATCGGCCATCATGCTTATAGTGAATAC      | 419  |            |      |        |    |      |    |
| Db      | 389  | TCCTCACTGGTTTATGGGTCTATGGGCCATGAATGGGCCATCATGCTTATAGTGAATAC      | 448  |            |      |        |    |      |    |
| Qy      | 420  | AGTGAATTGATAAACCGCGTTGGATTGCTGCTCCATTTGGCTCTCTGCTCAACCCCTTACTTTT | 479  |            |      |        |    |      |    |
| Db      | 449  | AGTGGGTTGATAAACACCGTTGGATTCTTCACTCTCCATTTCTTTCTTCACACCTTACTTTT   | 508  |            |      |        |    |      |    |
| Qy      | 480  | CTTGGAAATACAGCCATCGAAGACCAATGCAACACAAAATCTCACTCGAAACGAGGAG       | 539  |            |      |        |    |      |    |
| Db      | 509  | CTTGGAAATACAGCCATCGAAGACCAATGCAACACAAAATCTCACTCGAAGACGAGGAG      | 568  |            |      |        |    |      |    |
| Qy      | 540  | TTTACATTTCTTAGAACTCAGTCCCACTCAGGACTTACTCCACATACGAATTTCTTGACA     | 599  |            |      |        |    |      |    |
| Db      | 569  | TTTACATTTCTTAGAACTCAGTCCCACTCAGGACTTACTCCCAATTTCAAAATTTCTTGACA   | 628  |            |      |        |    |      |    |
| Qy      | 600  | ACACGCTGGTGGAAATCCTCATCTTGGTGCATCATGTTAAACCTTAGGATTTCTCTTTATACC  | 659  |            |      |        |    |      |    |
| Db      | 629  | ACACGCTGGTGGAAATCCTCATCTTGGTGCATCATGTTAAACCTTAGGATTTCTCTTTATACC  | 688  |            |      |        |    |      |    |
| Qy      | 660  | TCCTTAACGAATGTTTCAGGCAAGAGTAGTAGATAGATTTTACCAACACCTTTGCATCATTTGA | 719  |            |      |        |    |      |    |
| Db      | 689  | TCCTTAACGAATGTTTCAGGCAAGAAATACCAAGGTTTGGCAACCACTTGAATCCGTTGA     | 748  |            |      |        |    |      |    |
| Qy      | 720  | GCCGATCTTCAACGAGCGGTGAGCGAAATCCAGGTTTGGCTTATCAGATCTTGGTATCGTTG   | 779  |            |      |        |    |      |    |
| Db      | 749  | GCCGATCTTCAACGAGCGGTGAGCGAAATCCAGGTTTGGCTTATCAGATCTTGGTATCGTTG   | 808  |            |      |        |    |      |    |
| Qy      | 780  | CAGTGTGTTTACCGGATCTCAAGTTTCTTGTATACAAACAAAGGATTTGGTGGGTGATGTGCA  | 839  |            |      |        |    |      |    |
| Db      | 809  | CTGTGTGTTTACCGGCTTAAAGTTTCTTGTAGCGAAAGGTTTGGTGGGTGATGTGCA        | 868  |            |      |        |    |      |    |
| Qy      | 840  | TGATGGAATTTCCAGTGTAGTCTGAATTCCTTCATTTATCGTATCACTTTATCTCGACC      | 899  |            |      |        |    |      |    |
| Db      | 869  | TGATGGAATTTCCAGTGTAGTCTGAATTCCTTCATTTATCGTATCACTTTATCTCGACC      | 928  |            |      |        |    |      |    |
| Qy      | 900  | ACACATCTGTCTGTACGCCATTAACGATTCGAATTCGAATTCGAATTCGAATTCGAATTCGA   | 959  |            |      |        |    |      |    |
| Db      | 929  | ACACCATCTGTCTGTACGCCATTAACGATTCGAATTCGAATTCGAATTCGAATTCGAATTCGA  | 988  |            |      |        |    |      |    |
| Qy      | 960  | TGACCAATACGACAGAGATTTGGTCTCTGTAATTCGGGTTTTTCCAGCGTTTACACACA      | 1019 |            |      |        |    |      |    |
| Db      | 989  | TGACTACAATACGATAGAGATTTGGGCTCTCTGTAATTCGGGTTTTTCCAGCGTTTACACA    | 1048 |            |      |        |    |      |    |
| Qy      | 1020 | CCACGTTGTGACCATTTGTTTCCCTACATTTCCACATTTATCATGCAAGGAGGCAAGCG      | 1079 |            |      |        |    |      |    |
| Db      | 1049 | CACACGTTGTGATCATTTGTTTCCCGTACATTTCCACATTTATCATGCAAGGAGGCAAGCG    | 1108 |            |      |        |    |      |    |
| Qy      | 1080 | AGGCCATCAAGCCAAATCTTGGGTGATTAACGATGATCGACAGGACTCCATTTTTTCAAG     | 1139 |            |      |        |    |      |    |
| Db      | 1109 | AGCCAAATAGCCCGGTGTTAGGGAGTATCGATGATCGATGAGTCTCCGTTTTTACAAAG      | 1168 |            |      |        |    |      |    |
| Qy      | 1140 | CAATGTGAGAGAGGCCAAGGAATGCAATTTATCGAGCAGATGTCAGACAGCAGACACA       | 1199 |            |      |        |    |      |    |
| Db      | 1169 | CAATGTGAGAGAGAGGCCAAGGAATGCAATTTATCGAGCAGATGTCAGACAGCAGACACA     | 1228 |            |      |        |    |      |    |





Db 719 GCGCGCGCTGGGTGACGTGCAATTTACGGAATCCAGTTTATAGCGGTGTTATCTTTTCG 778  
Qy 879 TCGTAATCACTTATCTGCACACACACATCTGTGTCGTCACCCATTACGATTCAACCGAAT 938  
Db 779 ATATCATCACTTACTTGCACACACACCCATCTGTGTCGCTCATATGATGATCTGAAT 838  
Qy 939 GGAATCGGATCAAGAGCGCTTGCACACCAATCGACAGAGATTTCGCTCTCTGAATCGG 998  
Db 839 CGAATCGGCTCAGAGGGCTTTGTCAACATCGATAGGACCTTGGGTTCTCTGAATAGT 898  
Qy 999 TTTTCCACACCTTACACACACCCAGCTGTTCGACCAATTTGTTCCCTACATTCACAT 1058  
Db 899 TGTCTCATGATGTTACACACATCACTGATGATGATGATGATGATGATGATGATGAT 958  
Qy 1059 ATCATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1118  
Db 959 ATCATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1018  
Qy 1119 ACAGGACTCCATTTTCAAGCAATGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1178  
Db 1019 ATAGGACTCCAATTTCAAGCAATGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1078  
Qy 1179 AGATGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1228  
Db 1079 CTGAAAAGGTAGGAGGAGTCAAGGGGTGATATTTGGTACAAATTAATTTCTGA 1128

## RESULT 5

US-09-133-962A-1

Sequence 1, Application US/09133962A

Patent No. 6372965

GENERAL INFORMATION:

APPLICANT: JONATHAN EDWARD LIGHTNER

TITLE OF INVENTION: GENES FOR MICROSMAL FATTY ACID

DELTA-12 DESATURASES AND RELATED

ENZYMES FROM PLANTS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95

SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/133,962A

FILING DATE: 14-Aug-1998

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 07/977,339

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNN M.

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1043-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)992-5481

TELEFAX: (302)773-0164

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:  
CLONE: p92103  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93..1244  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-133-962A-1

Query Match 30.3%; Score 426.2; DB 3; Length 1372;

Best Local Similarity 61.0%; Pred. No. 4.1e-107;  
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

Qy 65 TTCAGAAATCTGGGAGAGGTAGCAGAATGTCGGGATTCATATGATGATGATGATGATGAT 124  
Db 84 TCCAGAAATCTGGGAGAGGTAGCAGAATGTCGGGATTCATATGATGATGATGATGATGAT 143  
Qy 125 CATGATATGGACGAAACGAGCCCCGATGATCGGCGCCATTCCTGTTAAGTATGATCTAAAG 184  
Db 144 ACCGACACCAAAACGCGTGTGCGGTGCGAGAAACCGCCCTTCTCGGTGGGAGATCTGAAG 203  
Qy 185 AAAGCAATCCCTGACATGTTTCCGGCGATCCGCGGTCTGCTCATCTCTGCTACGATGTT 244  
Db 204 AAAGCAATCCCGCGCATTTGTTTCAACGCTCAATCCCTCGCTCTTCTCTACCTTATC 263  
Qy 245 CAGGATCTCATTTATACACGCTTCTTTTATACAGGTGCGCAACACCTTACATTTCTCACTC 304  
Db 264 AGTGACATCATTTATAGCCTCATGCTTCTACTAGTCGCGCCACCAATTTCTCTCTCTC 323  
Qy 305 CCTCTCTCTTAGTTTACTTAGCATGGCGGTTTACTGGTGTGTTTGGCAATCTTTGCACTCTC 364  
Db 324 CCTCAGCCTCTCTTACTTGGCTTGGCCACTCTATTGGCGCTGTCAAGGCTGTGCTCTA 383  
Qy 365 ACTGTTTATGGTCTCGGCCATGAATGCGGCCATCATGCTTTAGTGAGTACGATGG 424  
Db 384 ACTGGTATCTGGGTATAGCCCAACGAATCGGTGTCACGACGATTCAGCGACATACCAATG 443  
Qy 425 ATTGATAAGCGGTGGATTGCTCTCCATTCGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 484  
Db 444 CTGGATGACACAGTTGGTCTTATCTTCCANTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 503  
Qy 485 AAATACAGCCATCGAAAGCACCATGCAAAACAAATTTCACTCGAAACAGGAAAGTTTAC 544  
Db 504 AGTATAGTCATCGCGCTGACCATTTCCAAACACTGGATCCCTCGAAAGAGATGAAGTATT 563  
Qy 545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATAGCAATTTCTTGACAAACAG 604  
Db 564 GTCCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAAATAC-----CTCAACACCCCT 617  
Qy 605 CTGTGCGAATCCTCATCTTGTGTCATCATGTTAACTTAGGATTTCTTTTATACCTTTA 664  
Db 618 CTGGACGATCATGATGTTAACTGTCAGTTTGTCTGCGGTGGCGCTTGTACTTAGCC 677  
Qy 665 ACGAATGTTTTCAGGCAAGAGTACGATAGATTTTACCAACACTTTTGATCCATTTAGCCCG 724  
Db 678 TTTAAGCTCTTGGCAGACCGGTATGACGGTTGCGTTGCGCATTTCTTCCCAACCGTCCC 737  
Qy 725 ATCTTTCACGAGCGTGAGGAAATCAGGTTGCGTTTATCAGATCTTGGTATGCTTGGAGTG 784  
Db 738 ATCTAATGACCGAGAACCGCTCCAGATATACCTCTCTGATGCGGGTATTCTAGCCGTC 797  
Qy 785 TTTTACGACTCAAGTTTCTTGTACAAACAAAGAGTTTGGTGGGTGATGTCATGAT 844  
Db 798 TGTGTTGCTTTTACCGTTACGCTGTCGCAAGGAGTGGCTCGATGATCTGCTCTAC 857  
Qy 845 GGAGTTTCCAGTGTAGGTTCTGAATTTCTTCAATTTCTTAATCACTTATCTGACCAACACA 904  
Db 858 GGAGTACCGCTCTGATAGTGAATGGTTCCTGCTCTGCTGATCACTTACTTGGAGCACACT 917  
Qy 905 CATCTGCTCACCCCATTTACGATTTCAACCGAATGGAATGGAATCAAGAGCGCTTGACC 964

Db 918 CATCCCTGTTGCTCACTACGATTCATCAGAGTGGGACTGGCTCAGGGGAGCTTTGGCT 977  
Qy 965 ACAATCGACAGAGATTTCCGCTCTCTGAATCCGGTTCACAGAGTTCACACACACCCAC 1024  
Db 978 ACCGTAGACAGAGACTCGGAATCTTGAACAAGGTGTTCCACAACATTCACAGACACAC 1037  
Qy 1025 GTGTTGCAACATTTGTTTCCCTACATTCACATTCATATCATGCAAGGAGGCAAGGAGGCC 1084  
Db 1038 GTGGCTCATACCTGTTCTCGACAATGCCGATTATACGCAATGGAAGCTTACAAAGGCG 1097  
Qy 1085 ATCAAGCCAACTTGGGTGATTACAGGATGATCGACAGGCTCCATTTTTCAAAGCAATG 1144  
Db 1098 ATAAAGCCAACTTGGGAGACTTATACCAAGTTCGATGGAACACCGTGGTATGTAGCGGATG 1157  
Qy 1145 TGGAGAGGCGCAAGGAATGATTTACATCGAGCAAGATGACAGACAGCAAGCAAAAGGG 1204  
Db 1158 TATAGGAGGCAAGGAGTGTATCTATGTAGACCGGACAGGAGGTGACAAGAAAGGT 1217  
Qy 1205 ACATATCGTACCAATAAATGTAAT 1229  
Db 1218 GTGTAAGTGGTACCAATAAAGTTAT 1242

RESULT 6  
US-09-763-331-5  
; Sequence 5, Application US/09763331  
; Patent No. 6825335  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Charles E.  
; APPLICANT: Mitchell, Andrew  
; TITLE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for  
; FILE REFERENCE: 97-0081 PCT  
; CURRENT APPLICATION NUMBER: US/09/763,331  
; PRIOR FILING DATE: 1999-08-24  
; PRIOR FILING DATE: 1998-08-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: SeqSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1372  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-763-331-5

Query Match 30.3%; Score 426.2; DB 3; Length 1372;  
Best Local Similarity 61.0%; Pred. No. 4.1e-107;  
Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

Qy 65 TTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTCATATGATGATCGAATGAAAGAT 124  
Db 84 TCCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTCATATGATGATCGAATGAAAGAT 143  
Qy 125 CATGATATGGAAGCAAGAGCCCGGATGATCGGCGGCAATCTCTGTTAAGTATCTAAAG 184  
Db 144 ACCGACACCAAAAGCGTGTGCGGTGCGAGAAACCGCCTTTCTCGGTGGGAGATCTGAAG 203  
Qy 185 AAAGCAATCCCTGACATGTTCTCGGCGATCGGCGCTGTCATCTGCTAGCTAGT 244  
Db 204 AAAGCAATCCCGCCGATGTTTCAAAAGCTCAATCCCTCGCTCTTTCTCTACCTTATC 263  
Qy 245 CAGGATCTCATTCATCCTCTCTTTTATACAGGTCGCGCAACACCTACATTCCTCACCTC 304  
Db 264 AGTGACATCATTTATAGCTCATGCTTCTACTAGTCGCGCAACATTTCTCTCTCTCTC 323  
Qy 305 CCTCTCTCTAGTTTACTAGCATGGCGGTTTACTGGTTTGGCAATCTTTGCAATCTCTC 364  
Db 324 CCTCAGCTCTCTCTTACTTGGCTTGGCCACTCTATTTGGGCTGTCAAGGCTGTGCTCTA 383  
Qy 365 ACTGGTTTATGGTCTCGGCCATGATCGGCCCATCATGCTTTAGTGAGTACCAGTGG 424  
Db 384 ACTGGTATCTGGGTCAATAGCCCAAGCAAGATCGGTACACGCAATTCAGCGACTTACCAATGG 443

Qy 425 ATTGATTAACGCCGTTGATTCGTCCTCAATTCGGCTCTCTCACCCTTACTTTTCTTGG 484  
Db 444 CTGATGACACAGTTGGTCTTATCTTCCATTCCTTCTCTCGTCCCTTACTTCTCTCGG 503  
Qy 485 AATACAGCCCATCGAAGCAGCAATGCAAAACACAAATTCACTCGAAAACGAGGAAGTTTAC 544  
Db 504 AAGTATAGTATCGCCCTCACCATTCCACATCGGATTCGATCCCTCGAAGAGATGAAGTATTT 563  
Qy 545 ATTCCTAGAACTCAGTCCCGAGCTCAGGACTTACTCCACATACATACGAATTTCTTTGACAACACG 604  
Db 564 GTCCCAAGCAGAAATCAGCAATCAAGTGTGACGGAATAC-----CTCAACAACCT 617  
Qy 605 CTGGTTCGAATCTCATCTTGGTTCATCATGTTAACTTAGAATTTCTTTTACTCTCTTA 664  
Db 618 CTGGAGCGCATCATGATGTTAAACCGTCCAGTTTGTCTCGGGTGGCCCTTTGTACTTAGCC 677  
Qy 665 ACGAATCTTTCAGGCAAGAAAGTACGATAGATTTTACCAACCACTTTTGATCCATTGAGCCCG 724  
Db 678 TTTAACGTCTCTGGCAGACCGGTATGACGGTTCGCTTGCCATTTCTTCCCAACGCTCCC 737  
Qy 725 ATCTTCAACGAGCGTGAGCGAATCCAGGTTGCGTTTATCAGATCTTGGTATCGTTCAGTG 784  
Db 738 ATCTAATGACCGAGAAACGCTCCAGATATACCTCTCTGATGCGGTATTTCTAGCCGTC 797  
Qy 785 TTTTACCGGACTCAAGTTTCTTTGTACAAACAAAGGATTTGGTGGGTGATGTGATGTAT 844  
Db 798 TGTCTTGGTCTTTACCGTTAGCGTGTGCAACAGGATGCGCTCGATGATCTGCTCTCTAC 857  
Qy 845 GGAGTTCAGTATAGTCTCAATTCCTTCATATCGTAACTTATCGTAACTTATCGCACCACACA 904  
Db 858 GGAGTACCGCTTCTGATAGTAAATGCGTTCCTGCTTTGATCACTTACTTTCACGACACT 917  
Qy 905 CATCTGCTGCACCCCATTCAGATTCAACCGAATGGAATCGAATCGAATCGAATCGAATCGA 964  
Db 918 CATCCCTGTTGCTCTACTAGATTATCAGAGTGGGACTGGCTGGCTCAGGGAGCTTTGGCT 977  
Qy 965 ACAATCGACAGAGATTTCCGCTCTCTGAATCGGTTTTCACGAGCTTTTACACACACCCAC 1024  
Db 978 ACCGTAGACAGAGACTACGGAATCTTGAACAAGGTGTTTCCACAACATTTACAGACACAC 1037  
Qy 1025 GTGTTGACCAATTTGTTTCCCTACATTCACATTCATTCGAAAGGAGGCAAGGAGGCC 1084  
Db 1038 GTGGCTCATCACCTGTTCTCGACAAATGCCGATTAACGCAATGGAAGCTTACAAAGCG 1097  
Qy 1085 ATCAAGCAATCTTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCAAAGCAATG 1144  
Db 1098 ATAAAGCCAACTTCTGGGAGACTTATACCAAGTTCGATGGAACACCGTGTGTATGAGCATG 1157  
Qy 1145 TGGAGAGGCGCAAGGAATGCAATTTACATCGAGCAAGATGACAGACAGCAAGCAAAAGGG 1204  
Db 1158 TATAGGAGGCAAGGAGTGTATCTATGTAGAACCGGACAGGAGGTGACAAGAAAGGT 1217  
Qy 1205 ACATATGTTTACCAATAAATGTAAT 1229  
Db 1218 GTGTAAGTGGTACCAATAAAGTTAT 1242

RESULT 7  
US-09-697-379-1  
; Sequence 1, Application US/09697379  
; Patent No. 6872872  
; GENERAL INFORMATION:  
; APPLICANT: JONATHAN EDWARD LIGHTNER  
; APPLICANT: JOHN JOSEPH OKULEY  
; TITLE OF INVENTION: GENES FOR MICROSOIAL  
; DESATURASES AND RELATED  
; ENZYMES FROM PLANTS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS  
; AND COMPANY



STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Microsoft Word Version 7.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/697,379

FILING DATE: 26-Oct-2000

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 07/977,339

FILING DATE: 17-NOV-1992

APPLICATION NUMBER: U.S. 09/133,962

FILING DATE: 14-AUG-1998

## ATTORNEY/AGENT INFORMATION:

NAME: Christenbury, Lynne M.

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: B01043 US DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-5481

TELEFAX: (302) 892-1026

TELEX: 835420

## INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Arabidopsis thaliana

IMMEDIATE SOURCE:

CLONE: p92103

## FEATURE:

NAME/KEY: CDS

LOCATION: 93..1244

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-697-379-1

Query Match 30.3%; Score 426.2; DB 3; Length 1372;

Best Local Similarity 61.0%; Pred. No. 4.1e-107;

Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

QY 65 TTCAGAAATCTGGGAGAGTAGCAGAAATGTCGGATTTCATATGATGATCGAATGAAAGAT 124

DB 84 TCAGAAACATGGTGCAGGTGAAGAAATGCCGGTTCCTACTTCTTCCAGAAATCGGAA 143

QY 125 CATGATATGGACGAACGAGCCCGATTGATCCGGCGCCATTCCTGTTAAAGTGAATCAAAG 184

DB 144 ACCGACACCAAAAGCGTGTCCGTCGGAGAAACCGCTTCTCGGTGGGAGATCTGAAG 203

QY 185 AAGCAATCCCTGCAATTCCTTCGGCGGATCCGGCGATCCGGTCTGTCATCTCTGCTACGTAGT 244

DB 204 AAGCAATCCCGCGCATTTGTTTCAAAACGCTCAATCCCTCGCTCTTCTCTCTACCTTATC 263

QY 245 CAGGATCTCATATACCTTCTTTTATACAGGTCGCCAAGACCTACATTCCTCTACCTC 304

DB 264 AGTGACATCATATAGCCTCATGCTTCTACTAGTCGCCAACCACCAATTACTTCTCTCTCCTC 323

QY 305 CTTCTCTCTCTAGTTTACTTAGCATGCGCGTTTACTGTTTGTGCAATCTTGCATCTCCTC 364

DB 324 CTTGACCTCTCTTACTTGGTGGCCACTATTTGGCCCTGTCAAGCTGTGTCCTA 383

QY 365 ACTGGTTTATGGTCTTCGGCCCATGAATCGGCCCATCATGCTCTTTAGTGAGTACCAAGTGG 424

DB 384 ACTGGTATCTGGTTCATAGCCCAAGAAATGCGGTCCACGAGCTTACGAGCACTACCAATGG 443

QY 425 ATTGATAACGCCGTTGGATTTCCTCTCCATTCGGCTCTCTCACCCCTTACTTTTCTTGG 484

DB 444 CTGGATGACACAGTTGGTCTTATCTCCATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 503

QY 485 AATATACAGCATCGAAAGCACCATCGAAACAAATTCATCTCGAAACGAGAAAGTTTAC 544

DB 504 AAGTATAGTCATCGCGCTGACCAATTCACACTGGATCCCTCGAAAGAGATGAAGTATTT 563

QY 545 ATTCTAGAAATCAGTCCCGAGCTCAGGACTTACTCCACATAGCAATTTCTTGACACACG 604

DB 564 GTCCCAAGCAGAAATCAGCATCAAGTGTACGGGAATAC-----CTCACAAACCT 617

QY 605 CTTGTCGAATCCTCATCTTGGTTCATGTTTAACTTAGGATTTCTTTTATACCTTTA 664

DB 618 CTTGACGCGATCATGATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 677

QY 665 AGCAATGTTTTCAGGCAAGAGTACGATAGATTTTCAACCACTTTTGCATTCATTTAGCCCG 724

DB 678 TTTAACTGCTCTGCGCAGACCGGATGACGGTTTCTGCTTCTTCTTCTTCTTCTTCTTCT 737

QY 725 ATCTTTCACCGAGCTGAGCAATTCAGGTTGCGTTTATCAGATCTTGGTATCGTTGAGTG 784

DB 738 ATCTAATGACCGAGAGCGCTCCAGATATACCTCTCTGATGCGGGTATTTCTAGCCGTC 797

QY 785 TTTTACGAGCTCAAGTTTCTTGTACAAACAAAGAGTTTGGTTGGGTGATGTGATGTAT 844

DB 798 TGTCTTGGTCTTTTACCGTTTACGCTGTCGCAAGGATGCGCTCGATGATCTGCTCTTAC 857

QY 845 GGAGTTCAGTATAGTCTGAATTCCTTCAATTCGATTCATCTTCTGATGCGGGTATTTCTAGCCGTC 904

DB 858 GGAGTACCGCTTCTGATAGTGAATGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 917

QY 905 CATCTGTGTCACCCCATTTACGATTTCAACCGAATGGAATCGGATCAAGAGAGCTTGACC 964

DB 918 CATCCCTGTTGCTCTCATGATTTTCAAGTTCAGAGTGGGACTGGCTCAGGGAGCTTTGGCT 977

QY 965 ACAATCGACAGAGATTTTCGGTCTCTCTGAATCGGGTTTTTCCACGAGCTTACACACCCAC 1024

DB 978 ACCGTAGACAGAGACTACGGAATCTTGAACAAAGGTGTTCCACAACTTACAGACACAC 1037

QY 1025 GTGTTGCACTTTGTTTCCCTACATTCACATTCATTCGAAAGAGGCAAGCGAGGCC 1084

DB 1038 GTGGCTCATCACTCTTCTCGCAATTCGCGCATTTAAGCGAATGGAAGCTTACAAAGCG 1097

QY 1085 ATCAAGCCCAATCTCGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATG 1144

DB 1098 ATAAAGCCCAATCTCGGAGACTTATACAGTTCGATGGAAACCCGTTGGTATGTAGCGATG 1157

QY 1145 TCGAGAGAGGCCCAAGGAATGCAATTTTACATCGAGCAAGATGACAGACGCAAGCAAGAGG 1204

DB 1158 TATAGGAGGCAAGAGGTGATCTTATGTAGAACCGGACAGGAGGTGCAAGAAAGGT 1217

QY 1205 ACATATGCTACATAAATGTAAT 1229

DB 1218 GTGTACTGTCACAAATAAGTTAT 1242

## RESULT 8

US-10-116-212A-1

; Sequence 1, Application US/10116212A

; Patent No. 6919466

; GENERAL INFORMATION:

; APPLICANT: JONATHAN EDWARD LIGHTNER

; JOHN JOSEPH OKULEY

; WILLIAM DEAN HITZ

; ANTHONY JOHN KINNEY

; NARENDRA YADAV

; LUIS PEREZ-GRAU

; TITLE OF INVENTION: GENES FOR MICROSOMAL

; FATTY ACID DELTA-12

; DESATURASES AND

; HYDROXYLASES FROM PLANTS

NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Dell  
OPERATING SYSTEM: Windows 2000  
SOFTWARE: Microsoft Word 97 SR-2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/116,212A  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 09/697,379  
FILING DATE: 26-OCT-2000  
APPLICATION NUMBER: U.S. 09/133,962  
FILING DATE: 14-AUG-1998  
APPLICATION NUMBER: U.S. 08/262,401  
FILING DATE: 20-JUN-1994  
APPLICATION NUMBER: PCT/US93/09987  
FILING DATE: 15-OCT-1993  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Christenbury, Lynne M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB1043USDIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-5481  
TELEFAX: (302) 892-1026  
TELEX: 835420

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1372 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:  
CLONE: p92103  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93..1244  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-116-212A-1

Query Match 30.3%; Score 426.2; DB 3; Length 1372;

Best Local Similarity 61.0%; Pred. No. 4.1e-107;

Matches 711; Conservative 0; Mismatches 448; Indels 6; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| QY | 65  | TTCCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTTCATATGATCGATGAAAGAT | 124 |
| DB | 84  | TCGAGAAACATGGGTGCGAGGTGGAAGATGCGGTTCTTCTTCCAGAAATCGGAA     | 143 |
| QY | 125 | CATGATATGAGCAACGAGCCCGATTGATCGGCGCCATTCTCGTTAAGTGATCTAAAG  | 184 |
| DB | 144 | ACCGACACCAAAAGCGGTGCGGTGCGGAAACCGCCTTCTCGGTGGAGATCTGAAG    | 203 |
| QY | 185 | AAAGCAATCCCTGCAATTGCTTCGGGGATCCGCGCTGTGTATCTGTCTACGTAGTT   | 244 |
| DB | 204 | AAAGCAATCCCGCGCAATGTTTCAAAAGCTCAATCCCTCGCTCTTCTCTACCTTATC  | 263 |
| QY | 245 | CAGGATCTCATTTACCTTCTTTTATATACAGGTCGCCAACACCTACATTTCTCACCTC | 304 |

|    |      |  |      |
|----|------|--|------|
| DB | 264  | AGTGACATGATTATAGCTTCATGCTTCTACTAGTCGCCACCAATTACTTCTCTCTCCT   | 323  |
| QY | 305  | CTCTCTCTCTAGTTTACTTAGCATGGCCGGTTTACTGGTTTGGCCAACTTGTGATCCTC  | 364  |
| DB | 324  | CCTCAGCCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGTCTTA    | 383  |
| QY | 365  | ACTGGTTTATGGGCTCTCGGCCATGAATGGGCCATCATGCTTATAGTACCACTGG      | 424  |
| DB | 384  | ACTGGTATCTGGGTTCATAGCCACGAATGGGTGACCAACGATTCACGCACTACCAATG   | 443  |
| QY | 425  | ATTGATAACCGCGTTGGATTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT    | 484  |
| DB | 444  | CTGATGACACAGTTGGTCTTAICTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT    | 503  |
| QY | 485  | AAATACAGCCATCGAAAGACCAATGCAAAACAAATTCATTCGAAAAAGGAGATTTAC    | 544  |
| DB | 504  | AAGTATAGTCATCGCGCTCACCATTCACATCGATCCCTCGAAAGAGATGAAGTATTT    | 563  |
| QY | 545  | ATTCCTAGAACTCAGTCCAGCTCAGCACTTACTCCACATACGAAATTTCTTGACAACG   | 604  |
| DB | 564  | GTCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACAAACCT    | 617  |
| QY | 605  | CCTGCTCGAATCCTCATCTTGGTCATCATGTTAACTTAGGATTTCTTTATACCTCTTA   | 664  |
| DB | 618  | CTTGACGCAATCATGATGTTAAACGTCAGTTTGTCTCTCGGTGGCCCTTGTACTAGCC   | 677  |
| QY | 665  | ACGAATGTTTCAGCAAGAGTAGTAGATTTTACCAACCACTTTGATTCATTTGAGCCG    | 724  |
| DB | 678  | TTTAAACGCTCTGGCAGACCGTATGACGGGTTGCTTTGCCATTTCTTCCCAACGCTCC   | 737  |
| QY | 725  | ATCTTACCGAGCGTGAGCAATCCAGTTGCGTTATCAGATCTTGTATGTTGCGAGTG     | 784  |
| DB | 738  | ATCTTCAATGACCGAGAACCGCTCCGATATACCTCTCTGATGGGGTATTTCTAGCCGT   | 797  |
| QY | 785  | TTTTACCGACTCAAGTTTCTTGTAACAAACAAAGGATTTGGTTGGGTGATGTCATGTAT  | 844  |
| DB | 798  | TGTTTGGTCTTTACCGTTACGCTGCTGCACAGGGATGGCTCGATGATCTGCTCTAC     | 857  |
| QY | 845  | GGAGTTCCAGTGATAGGTCTGAATTCCTTCAATATCGTATCATTTCTGACACACACA    | 904  |
| DB | 858  | GGAGTACCGCTTCTGATAGTGAATGCGTTCTCTGCTTTGATCACTTACTTGCAGCACT   | 917  |
| QY | 905  | CATCTGCTGCACCCCATTAAGATTCAACGAATGGAATGGATCAAGAGAGCCTTGACC    | 964  |
| DB | 918  | CATCCCTGTTGCTCTACATGATTCAGAGTGGGACTGGCTCAGGGGAGCTTTGGCT      | 977  |
| QY | 965  | ACAATGACAGAGATTTTCGGTCTCTCGAATCGGGTTTTTCCACGACGTTTACACACCCAC | 1024 |
| DB | 978  | ACCGTAGACAGAGACTAGGNAATCTTGACNAAGGTGTTCCACACATTTACAGACACAC   | 1037 |
| QY | 1025 | GTGTTGCAACATTTGTTTCCCTACATTCACATTTATCATGCAAAAGGAGGCAAGGAGCC  | 1084 |
| DB | 1038 | GTGGCTCATCACCTGTTCTCGACAATGCGCATTAACGCAATGGAAGCTTACAAAGCG    | 1097 |
| QY | 1085 | ATCAAGCAATCTTGGGTGATTACAGGATGATCAGAGGACTCCATTTTCAAAGCATG     | 1144 |
| DB | 1098 | ATNAAGCAATTTCTGGGAGACTATTACAGTTCCATGGAACACCGTGGTATGTAGCGATG  | 1157 |
| QY | 1145 | TGGAGAGAGGCAAGGATGCAATTTATCATCGAGCAAGATGACAGACAGCAACCAAGGG   | 1204 |
| DB | 1158 | TATAGGAGGCAAGGAGTGTATCTATGTAGAACCGGACAGGAGGTGACAGAAAGGT      | 1217 |
| QY | 1205 | ACATTTGGTACCAATAAATGTAAT                                     | 1229 |
| DB | 1218 | GTGACTGGTACAAACAATAAGTTAT                                    | 1242 |

## RESULT 9

US-09-133-962A-15  
; Sequence 15, Application US/09133962A  
; Patent No. 6372965  
; GENERAL INFORMATION:

APPLICANT: JONATHAN EDWARD LIGHTNER  
JOHN JOSEPH OKULEY  
TITLE OF INVENTION: GENES FOR MICROSMAL FATTY ACID  
DELTA-12 DESATURASES AND RELATED  
ENZYMES FROM PLANTS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/133,962A  
FILING DATE: 14-Aug-1998  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHRISTENBURY, LYNNE M.

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1043-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)992-5481

TELEFAX: (302)773-0164

TELEX: 835420

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2973 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana

IMMEDIATE SOURCE:

CLONE: pAF2-6

FEATURE:

NAME/KEY: exon

LOCATION: 433..520

FEATURE:

NAME/KEY: intron

LOCATION: 521..1654

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-133-962A-15

Query Match 30.2%; Score 424.6; DB 3; Length 2973;  
Best Local Similarity 60.9%; Pred. No. 1.6e-106;  
Matches 710; Conservative 0; Mismatches 449; Indels 6; Gaps 1;  
65 TTCAGAAATCTGGGAGAGTACGAGATGTGCGATTTCATATGATGATCGAATGAAAGAT 124  
1650 TGCAGAAACATGGGTGAGTGGAGATGCGGTTCTTCTTCCAGAAATCGGAA 1709  
125 CATGATATGGACGAGAGCCCGATTGATCGGCGCGATTCTCGTTAAGTATCTTAAG 184  
1710 ACCGACACCAAAAGCGTGGCGTCGAGAAACCGCCCTTCTCGGTGGAGATCTGAAG 1769  
185 AAAGCAATCCCTGCACATTGCTTCCGCGGATCGCGCTCTGGTCACTCTGCTACGTAATT 244  
1770 AAAGCAATCCCGCGATTGTTTCAACGCTCAATCCCTCGCTCTTCTTCTTACCTTATC 1829  
245 CAGGATCTCATATCACTTCTCTTTTATACAGGTGCGCAACACCTTACATTCCTCACCTC 304

Db 1830 AGTGACATCATATAGCCTCATGCTTCTTACTAGTCGCGCCACCAATTACTTCTCTCTC 1889  
QY 305 COTCTCCTCTAGTTTACTTAGCATGGCCGTTTACTGGTTTTCGAATCTTTCGATCCTC 364  
Db 1890 CCTCAGCCTCTCTCTTACTTGGCTTGGCCACTCTATTGGCGCTGTCAAGGCTGTCTCTA 1949  
QY 365 ACTGGTTTATGGTCTCTGGCCATGAATCGGCCCATCATGCTTTTAGTGAGTACAGTGG 424  
Db 1950 ACTGGTATCTGGTTCATAGCCCAAGATCGCGTCCACGCAATTCAGGACTTACCAATGG 2009  
QY 425 ATTGATAACGCGTTGGATTGCTCTCCATTCTGGCTCTCTCACCCCTTACTTTTCTTGG 484  
Db 2010 CTGGATGACAGTGGTCTTATCTTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2069  
QY 485 AAATACAGCCATCGAAAGCAACATCAACAAACAAATCACTCGAAAGAGAGAGTGTAC 544  
Db 2070 AAGTATAGTATCGCGCTCACCATTCCAACACTGGATCCCTCGAAAGAGATGAAGTATT 2129  
QY 545 ATTCCTAGAACTCAGTCCAGCTCAGGACTTACTTCCATAGCAATTTCTTGACACAGC 604  
Db 2130 GTCCCAAGCAGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACAC 2183  
QY 605 COTGGTCGAATCCTCATCTTGGTTCATGTTTAACTTAGGATTTCTTTTATACCTCTTA 664  
Db 2184 CTGGACGATCATGATGTTAACCGTCCAGTTTGTCTCGGTGCGCTTGTACTTAGCC 2243  
QY 665 ACGAATGTTTCAGGCAAGAAGTACGATAGATTACCAACCACTTTTGATCCATTGAGCCG 724  
Db 2244 TTTAAGCTCTCTGGCAGACCGTATGACGGTTCGCTTGCCATTTCTTCCCAACGCTCC 2303  
QY 725 ATCTTACCGAGCGTGGAGGAATCCAGGTGGGTTTATCAGATCTTGGTATCGTTGAGTG 784  
Db 2304 ATCTACAATGACCGAGAACGCTCCAGATATACCTCTCTGATGCGGGTATTCTAGCCG 2363  
QY 785 TTTTACGAGCTCAAGTTTCTGTACAAACAAAGGATTGTTGGTGTGATGTCATGAT 844  
Db 2364 TGTTTGGTCTTTACCGTTACGCTGCTGCAAGGGATGGCTCGATGATCTGCTCTAC 2423  
QY 845 GGAGTTCAGTATAGGTCTGAATTTCTTCAATTCGTAATCACTTATCTGCACACACA 904  
Db 2424 GGAGTACCGCTTCTGATAGTGAATGCGTTCTCGTCTTGATCATTCTTGCAGACACT 2483  
QY 905 CATCTGCTCACCCCATTCAGATTCAACCGAATGGAATGGAATCAAGGAGCCTTGACC 964  
Db 2484 CATCCCTCGTTGCTCTCACTCAGATTTCATCAGAGTGGGACTGGCTCAGGGAGCTT 2543  
QY 965 ACAATCGACAGAGATTTCGGTCTCTGATCGGTTTCCAGAGCTTACACACACAC 1024  
Db 2544 ACCGTAGACAGAGACTACGGAATCTTGAAACAAAGGTGTTCCACAACTTACACACAC 2603  
QY 1025 GTTTGCAACATTTGTTTCCCTTACATTCACATTTATGCAAGGAGGCAAGCGGCC 1084  
Db 2604 GTGGCTCATCCTCTTCTCGACATTCGCGATTATACGCAATGGAAGCTACAAGGCG 2663  
QY 1085 ATCAAGCCAAATCTGGGTGATTCAGGATGATTCGACAGACTTCCATTTTTCAAAGCA 1144  
Db 2664 ATAAAGCCAAATCTCGGAGACTATTACCAAGTTCGATGGAACACCGTGTGATGTGG 2723  
QY 1145 TGGAGAGGCGCAAGCAATGCAATTTACATCGAGCAAGATGCAAGCAGCAGCAAGAGG 1204  
Db 2724 TATAGGAGGCGCAAGGAGTGTATCTATGTAGAACCGGACAGGGAAGGTGACAAAG 2783  
QY 1205 ACATATGCTACATAAAATGTAAT 1229  
Db 2784 GTGTACTGTACAAATAAGTTAT 2808

RESULT 10

US-09-697-379-15

; Sequence 15, Application US/09697379

; Patent No. 6872872

; GENERAL INFORMATION:

; APPLICANT: JONATHAN EDWARD LIGHTNER

JOHN JOSEPH OKULEY  
TITLE OF INVENTION: GENES FOR MICROSOMAL  
FATTY ACID DELTA-12  
DESATURASES AND RELATED  
ENZYMES FROM PLANTS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: E. I. DU PONT DE NEMOURS  
AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Microsoft Word Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/697,379  
FILING DATE: 26-Oct-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
APPLICATION NUMBER: U.S. 09/133,962  
FILING DATE: 14-AUG-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Christenbury, Lynne M..  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB1043 US DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-5481  
TELEFAX: (302) 892-1026  
TELEX: 815420

## INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2973 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:

CLONE: pGFP2-6

FEATURE:

NAME/KEY: exon

LOCATION: 433..520

FEATURE:

NAME/KEY: intron

LOCATION: 521..1654

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-697-379-15

Query Match 30.2%; Score 424.6; DB 3; Length 2973;  
Best Local Similarity 60.9%; Pred. No. 1.6e-106;  
Matches 710; Conservative 0; Mismatches 449; Indels 6; Gaps 1;  
QY 65 TTCAGAAATCTGGGAGAGGTTAGCAGAAATGTCGGATTCATATGATGATCGAATGAAAGAT 124  
Db 1650 TGCAGAAACATGGGTGCAGGTGGAAGAAATGCCGGTTCCTACTTCTTCCAGAAATCGGAA 1709  
QY 125 CATGATATGGACGACGAGCCCGGATTCATCGGCGCCATTCCTCGTTAAGTGATCTAAAG 184  
Db 1710 ACCGACACCAAAAGCGTGTGCGGCGGAGAACCGCCCTTCCTCGGTGGAGATCTGAAG 1769  
QY 185 AAAGCAATCCCTGCACATTCGTTCCGGCGGATCCGCCGTCTGGTTCATCTCTGCTACGTAGTT 244  
Db 1770 AAAGCAATCCCGCGCATTTGTTTCAAAACGCTCAATCCCTCGCTCTTTCTCTACCTTATC 1829

QY 245 CAGGATCTCTATTACCTTCCTTTTATACACGCTGCGCAACCTACATTTCTCACTC 304  
Db 1830 AGTGACATCATATAGCCCTCATGCTTCTACTAGCTGCCACCAATTAATTTCTCTCTCCTC 1889  
QY 305 CCTCCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTGGCCAAATCTTGATCCTC 364  
Db 1890 CTTAGGCTCTCTTACTTGGCTTGGCCACTCTATTGGGCTGTCAAGGCTGTGCTTA 1949  
QY 365 ACTGGTTTATGGGTCCTCGGCCATGAATGGGCCCATCATGCTTTAGTAGTACCACTGG 424  
Db 1950 ACTGGTATCTGGGTCATAGCCCAAGATGGGTCACCAACGATTTACAGGACTACCAATGG 2009  
QY 425 ATTGATAACGCGTGTGATTGCTCTCATTTGCGCTCTCTCAACCTTACTTTTCTTGG 484  
Db 2010 CTGGATGACACAGTTGGTCTTAATCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2069  
QY 485 AAATACAGCCATCGAAAGCACCATGCAAAACAAATTCATTCGAAAACGAGGAATTTTAC 544  
Db 2070 AAGTATAGTCATCGCCGTCACCATTCACACATGATCCCTCGAAAGAGATGAAGTATTT 2129  
QY 545 ATTCCTAGAACTCAGTCCCAGCTCAGGACTTACTCCACATACGAAATTTCTTGACAAACG 604  
Db 2130 GTCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAATAC-----CTCAACACCCCT 2183  
QY 605 CCTGGTCGAATCCTCATCTTGGTCATCATGTTAACTTAGATTTCTTTTATACCTCTTA 664  
Db 2184 CTGGACGCATCATGATGTTAACTGCTCGGTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2243  
QY 665 ACGAATGTTTCAGGCAAGAGTAGATAGATTTTACCAACCACTTTGATTCATTCAGCCG 724  
Db 2244 TTTAACTCTCTGGCAGACCGTATGACGGGTTGCTTTGCCATTTCTTCCCAACGCTCCC 2303  
QY 725 ATCTTACCAGCGTGAAGGAAATCCAGGTGCGGTTATCAGATCTTGGTATCGTTCGATG 784  
Db 2304 ATCTACAATGACCCGAGAACGCTCCAGATATACCTCTCTGATGCGGGTATTTCTAGCC 2363  
QY 785 TTTTACGGACTCAAGTTTCTTGTACAAACAAAGGATTTGGTTGGGTGATGTGATGAT 844  
Db 2364 TGTTTGGTCTTTTACCGTTACGCTGTGTCACAGGGATGGCTCGATGATCTGCTCTAC 2423  
QY 845 GGAGTTCGAGTATAGGTCTGAAATTCCTTCAATTCGTAATCACTTATCTGCACACACA 904  
Db 2424 GGAGTACGCTTCTGATAGTGAATGCGTTCCTCTCTTGTATCACTTACTTGCAGCACT 2483  
QY 905 CATCTGTGTCACCCCAATAGGATTCACCGAATGGAATGGATCGATCAAGAGGACCTTGAC 964  
Db 2484 CATCCCTCGTTGCTCTACATACGATTCATCAGAGTGGGACTGGCTCAGGGGAGCTTTGG 2543  
QY 965 ACAATCGACAGAGATTTGCTCTCGAATCGGGTTCCTCAACGAGCTTTTACACACACCCAC 1024  
Db 2544 ACCGTAGACAGAGACTACGGAAATCTTGAACAGGTGTTCCACAAATTTACAGACACAC 2603  
QY 1025 GTGTTGCACCAATTTGTTTCCCTACATTCACATTCACATTCATGCAAAAGGAGGAGGCC 1084  
Db 2604 GTGGCTCATCACCTGTTCTCGACAAATGCGCAATTAACGCAATGGAAGCTTACAAGCG 2663  
QY 1085 ATCAAGCCAATCTTGGGTGATTCAGGATGATCCAGAGGACTCCATTTTTCAAAGCAATG 1144  
Db 2664 ATAAAGCCAATCTTGGGAGACTATTACCAAGTTCGATGGAAACCCGCTGGTATGTGCGCAT 2723  
QY 1145 TGGAGAGAGCGCAAGGAATGCATTTTACATCCAGCAAGATGCAGACAGCAACGACAAAGGG 1204  
Db 2724 TATAGGAGGCAAGAGGAGTGTATCTATGTAGAACCGGACAGGGAAGGTGACAAAGGT 2783  
QY 1205 ACATATTGGTACCAATAAATGTAAT 1229  
Db 2784 GTGTACTGTTACAACTAAGTTAT 2808

RESULT 11  
US-10-116-212A-15  
; Sequence 15, Application US/10116212A

Patent No. 6919466  
GENERAL INFORMATION:  
APPLICANT: JONATHAN EDWARD LIGHTNER  
JOHN JOSEPH OKULEY  
WILLIAM DEAN HITZ  
ANTHONY JOHN KINNEY  
NARENDRA YADAV  
LUIS PEREZ-GRAU  
FATTY ACID DELTA-12  
DESATURASES AND  
HYDROXYLASES FROM PLANTS  
TITLE OF INVENTION: GENES FOR MICROSOEAL  
FATTY ACID DELTA-12  
DESATURASES AND  
HYDROXYLASES FROM PLANTS  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Dell  
OPERATING SYSTEM: Windows 2000  
SOFTWARE: Microsoft Word 97 SR-2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/116,212A  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 09/697,379  
FILING DATE: 26-OCT-2000  
APPLICATION NUMBER: U.S. 09/133,962  
FILING DATE: 14-AUG-1998  
APPLICATION NUMBER: U.S. 08/262,401  
FILING DATE: 20-JUN-1994  
APPLICATION NUMBER: PCT/US93/09987  
FILING DATE: 15-OCT-1993  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Christenbury, Lynne M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB1043USDIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-5481  
TELEFAX: (302) 892-1026  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2973 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:  
CLONE: pGFP2-6  
FEATURE:  
NAME/KEY: exon  
LOCATION: 433..520  
FEATURE:  
NAME/KEY: intron  
LOCATION: 521..1654  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-116-212A-15

Query Match 30.2%; Score 424.6; DB 3; Length 2973;  
Best Local Similarity 60.9%; Pred. No. 1.6e-106;

|    | Matches | 710;   | Conservative | 0; | Mismatches | 449; | Indels | 6; | Gaps | 1; |
|----|---------|--|--------------|----|------------|------|--------|----|------|----|
| QY | 65      | TTTCAGAAATCTCGGAGAGGTAGCAGAAATGTCGGATTTCATATGATGATCGAATGAAAGAT | 124          |    |            |      |        |    |      |    |
| DB | 1650    | TGCAGAAACATGGGTGCGAGTGAAGATGCGGTTCCTACTTCTTCCAGAAATCGGAA       | 1709         |    |            |      |        |    |      |    |
| QY | 125     | CATGATATGGACGAACAGAGCCCGATTGATCGGGGCCAATTCCTGTTAAGTATCTAAAG    | 184          |    |            |      |        |    |      |    |
| DB | 1710    | ACCGACACCAAAAGCGTGTGCGGAGAAACCGCTTCTCGGTGGAGATCTGAAG           | 1769         |    |            |      |        |    |      |    |
| QY | 185     | AAAGCAATCCCTGACATTCCTTCGGCGATCGCGCTGTGCTCATCTCTGCTACGTAGT      | 244          |    |            |      |        |    |      |    |
| DB | 1770    | AAAGCAATCCCGCGCATTTGTTTCAACGCTCAATCCCTCGCTCTTCTCTACCTATC       | 1829         |    |            |      |        |    |      |    |
| QY | 245     | CAGGATCTCATTTATCACCTTCTCTTTTATACCGGTGCGCAACACCTTACATTCCTCACTC  | 304          |    |            |      |        |    |      |    |
| DB | 1830    | AGTGACATCATTTATAGCCTCATGCTTCTACTAGTGCACCAATTTACTTCTCTCTC       | 1889         |    |            |      |        |    |      |    |
| QY | 305     | CCTCTCTCTAGTTTACTTAGCATGGCCGGTTTACTGTTTGGCAATCTTGCATCTTGCATCTC | 364          |    |            |      |        |    |      |    |
| DB | 1890    | CCTCAGCCTCTCTTACTTGGCTTGGCCACTCTATTTGGGCTGTCAAGGCTGTGTCCTA     | 1949         |    |            |      |        |    |      |    |
| QY | 365     | ACTGGTTTATGGTCTCTCGGCCATGAATCGCGCCATCATGCTTTAGTGAGTACCAAGTGG   | 424          |    |            |      |        |    |      |    |
| DB | 1950    | ACTGGTATCTGGGTATAGCCCAAGATGCGGTACCAGCAATTCAGCGACTACCAATGG      | 2009         |    |            |      |        |    |      |    |
| QY | 425     | ATTGATAACGCCGTTGGATTTCCTTCCATTCGGCTCTCCTCACCCCTTACTTTTCTTGG    | 484          |    |            |      |        |    |      |    |
| DB | 2010    | CTGGATGACAGTTGGTCTTATCTTCCATTCCTTCTCTCTCTCTCTCTCTCTCTCTG       | 2069         |    |            |      |        |    |      |    |
| QY | 485     | AAATACAGCCATCGAAAGCACCATGCAACAAATTCATCTGAAACAGAGAAAGTTTAC      | 544          |    |            |      |        |    |      |    |
| DB | 2070    | AAGTATAGTCATCGCGCTCACCAATTCACACTGGATCTCTGAAAGAGATGAAGTATTT     | 2129         |    |            |      |        |    |      |    |
| QY | 545     | ATTCTTAGAATCTAGTCCAGCTCAGGACTTACTCCACATCAGAAATTTCTTGACACAG     | 604          |    |            |      |        |    |      |    |
| DB | 2130    | GTCCCAAGACGAAATCAGCAATCAGTGGTACGGGAATAC-----CTCACACCCCT        | 2183         |    |            |      |        |    |      |    |
| QY | 605     | CTGGTTCGAATCTCATCTTGGTTCATCTTAACTTAACTTAACTTAACTTAACTTAACTT    | 664          |    |            |      |        |    |      |    |
| DB | 2184    | CTTGAGGATCATGATGTTTACCGTCCAGTTTGTCTCGGGTGGCCCTTGTACTTAGCC      | 2243         |    |            |      |        |    |      |    |
| QY | 665     | ACGAATGTTTTCAGGCAAGATGACGATAGATTTTCAACACCTTTGATTCATTTGAGCCCG   | 724          |    |            |      |        |    |      |    |
| DB | 2244    | TTTAACTCTCTGGCAGACCGTATACGGGTTCGCTTGCATTTCTTCCCAACGCTCCC       | 2303         |    |            |      |        |    |      |    |
| QY | 725     | ATCTTACCGAGGTGAGGCAATCCAGTTTACGATTCAGATCTTGGTATCGTTGCAAGTG     | 784          |    |            |      |        |    |      |    |
| DB | 2304    | ATCTAATATGACCGAGAACGCTTCCAGATATACCTCTCTGATCGGGTATTTAGCCGTC     | 2363         |    |            |      |        |    |      |    |
| QY | 785     | TTTTACGGAATCAAGTTTCTGTACAAACAAAGAGATTTGGTTGGGTGATGTGATGTAT     | 844          |    |            |      |        |    |      |    |
| DB | 2364    | TGTTTTGGTCTTTACCGTTACGCTGTCGCAAGGATGCGCTCGATGATCTGCTCTAC       | 2423         |    |            |      |        |    |      |    |
| QY | 845     | GGAGTTCAGTATAGTCTGAAATTCCTTTCATTTATCGTAATCATCTTATCTGCAACACAC   | 904          |    |            |      |        |    |      |    |
| DB | 2424    | GGAGTACCGCTTCTGATAGTGAATGCTTCTCTGCTTCTGATCACTTACTTTGAGCACT     | 2483         |    |            |      |        |    |      |    |
| QY | 905     | CATCTGCTCACCCTTACGATTCACCGAATGGAATGGAATGGAATGGAATGGAATGGAAT    | 964          |    |            |      |        |    |      |    |
| DB | 2484    | CATCCCTCGTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC     | 2543         |    |            |      |        |    |      |    |
| QY | 965     | ACAAATCGACAGATTTTCGTTCTCTGAAATCGGGTTTTCACGACGTTTACACACACCCAC   | 1024         |    |            |      |        |    |      |    |
| DB | 2544    | ACCGTAGACAGAGATACGGAATCTTGAACAGGTTTCCACAAATTTACAGACACACAC      | 2603         |    |            |      |        |    |      |    |
| QY | 1025    | GTGTTGCACTTGTGTTTCTTCCCTTACATTCACATTTATCATGCAAGAGGCAAGCGGCC    | 1084         |    |            |      |        |    |      |    |
| DB | 2604    | GTGGCTCATCCTCTGTTCTCGCAATGCGCATTTAAGCAATGGAAGCTACAAAGGCG       | 2663         |    |            |      |        |    |      |    |
| QY | 1085    | ATCAGCCCAATCTTGGGTGATTTACAGGATGATGACAGAGCTCCATTTTCAAGCAATG     | 1144         |    |            |      |        |    |      |    |
| DB | 2664    | ATAAGCCCAATTTCTGGGAGACTATTACAGTTTCGATGGAACACCGGTGATGTGGCGATG   | 2723         |    |            |      |        |    |      |    |

QY 1145 TGGAGAGGCGCAAGGAATGATTTACATCGAGCAAGATGAGACAGCAAGCAAGAGG 1204  
Db 2724 TATAGGAGGCAAGAGTGTATCTATGTAGAACCGGACAGGAGGTGACAAAGAGT 2783  
QY 1205 ACATATTGGTACCAATAAAATGTAAT 1229  
Db 2784 GTGTACTGGTACACAAATAGTTAT 2808

RESULT 12  
US-09-837-751-5  
; Sequence 5, Application US/09837751  
; Patent No. 6974898  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1422  
; TYPE: DNA  
; ORGANISM: Gossypium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (98)..(1246)  
US-09-837-751-5

Query Match 29.8%; Score 419.4; DB 4; Length 1422;  
Best Local Similarity 60.1%; Pred. No. 3.1e-105;  
Matches 718; Conservative 0; Mismatches 471; Indels 6; Gaps 1;  
QY 49 ATTTCTAATTTGGATTTTCAGAAATCTGGGAGAGGTAGCAGAAATGTCGGATTCAATATGA 108  
Db 73 ATCTCCATTTTAAAGGTTGGAACAAATGGTCTGGAGGAGAAATGTCGGTTCCAAACGAG 132  
QY 109 TGATCGAATGAAGATCATGATATGGACGACGACCGGATGATCGGCGCCATTCTC 168  
Db 133 TCCAAAANAACCCGAATTCACCTACTGAAGCGAGTTCCATACTCAAAAGCCACCCTTCAC 192  
QY 169 GTTAAGTGTATCTAAAGAAAGCAATCCCTGCACATTTGCTTCGGCGATCCGCGTCTGGTC 228  
Db 193 TCTGATGAAATCAAGAAAGCCATCCACCACTGTTTCCAGCGCTCGTTTACGCTC 252  
QY 229 ATCTCTGCTACGTTTCAGGATCTCATATACCTTCCTTTTATACAGCGTGGCCAAAC 288  
Db 253 ATTTCTCATATCTCTTTAGGACTTATATGCGCTCTCTTTTATACCATGTGGCCACCAA 312  
QY 289 CTACATTCCTACCTCCCTCTCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTG 348  
Db 313 TTACTTCCCTAACCTTCTCTCAGGCTCTCTCCAAAGCGGCTTGGCCTCTTTATTTGGGCCAT 372  
QY 349 CCAATCTTGATCTCTCCTCTCTCTGTTTATGGTCTCTCGGCCATGAATCGGCCATCATGCTT 408  
Db 373 GCAAGGTTGCAATTTGACCGGGGTTTGGTCTATGCCCATGAAATGGCCACCATGCTTT 432  
QY 409 TAGTGAGTACCAAGTGAATGAACCGCGTGGATTCGTCCTCCATTCGGCTCTCTCTCAC 468  
Db 433 CAGTGATTATCAATGGCTTGACGACACCGTGGGCTTATCTCCACTCTCTCTCTTAGT 492  
QY 469 CCCTTACTTTTCTTGGAAATACAGCCATCGAAGACCATGCAAAACAAATTCATCTCGA 528  
Db 493 TCCATATTTCTCTTGGAAATATAGCCACCGCGGTCAACCATTCGACACCGGTTCCCTCGA 552  
QY 529 AAACGAGGAAGTTTACATTTCTCTAGAACTCAGTCCCGAGCTCAGGACTTACTCCACATAGA 588

Db 553 AAGGGATGAAGTGTTCGTTCCCAAGAAAAAATCTGGTTTAAAGTGTGGGCGCAACAC-- 610  
QY 589 ATTTCTTGAACAACAGCGCTGGTCCGAATCCCTCATCTTGGTGTATCATGTATTAACCTTAGGATT 648  
Db 611 ----TTCAACAATCCACCGGGTCGGTTTCTGTCAATCACCATTCACTTACCTTGGTTG 666  
QY 649 TCCTTTATACCTCTTAACGAATTTTCAGGCAAGAAGTACGATAGATTTTACCAACCACTT 708  
Db 667 GCCGCTTTACTTAGCTTTCAAGTTTCGGCGCGGCTTACGACAGGTTTCGTTGCCACTA 726  
QY 709 TGATCCATTGAGCCCGATCTTTCACGAGCGGTAGCGAATCAGGTTTCGTTTATCAGATCT 768  
Db 727 TGACCTTTACGGCCCATATTTTCGACCGGGAACGACTCCAAATCTATATCTCTGACGC 786  
QY 769 TGGTATCGTTGCGAGTGTTCAGGACTCAAGTTTCTTGTGACAAACAAAGGATTTGGTTG 828  
Db 787 CGGCGTCTCGCTCGCTATCGCTCTACCGTCTCGTGTGGCCAAAGGGTGGTTG 846  
QY 829 GGTGATGTGATGATGAGTTCAGGTGATAGGTCTGAATTCCTTTCATTTATCGTAATCAC 888  
Db 847 GGTATTAGCGTTTATGGGTGCGCTTATTTGGTGTAAACGCTTCTTAGTAATGATCAC 906  
QY 889 TTATCTGCACCAACACATCTGTCTCACCCCATTTACGATTTCAACCGAATGGAATCGAT 948  
Db 907 GTATTTGCAACACACTCAACCATCTTTGCGCGCACTATGATTTCTCGGAGTGGACTGGAT 966  
QY 949 CAAAGGAGCCTTGACCAATCGACAGAGATTTCCGTTCTCTGAATCGGTTTTCACGA 1008  
Db 967 GAGAGGAGCTTTATCAACTGTGGACAGAGATTTATGGGATTTTAAACAAAGGTTTTCATAA 1026  
QY 1009 CGTTTACACACACCCACCGTTTGCACCATTTGTTTCCCTTACATTCACATTTATCATGCAAA 1068  
Db 1027 CATAAACGACACTCATGTGGCTCATCATTTGTTTTCGCAATGCTCTACTATCATGCAAT 1086  
QY 1069 GGAGGCAAGCGAGCCCATCAAGCCAATCTTGGGTGATTTACAGGATGATCGACAGACTCC 1128  
Db 1087 GGTGGCCACCAAGCGATATAAGCCCATATTTGGGGGAATCTATCAGTTCCGATGGATGCC 1146  
QY 1129 ATTTTCAAGCAATGTGGAGAGGCGCAAGGAATGCAATTTACATCGAGCAAGATGCGA 1188  
Db 1147 TGTCTATAAGCGATATGAGGAGGCGAAGGAGTGTCTCTACGTTGAACCAAGATGAGG 1206  
QY 1189 CAGCAAGCACAAGGACATATTTGTTACCAATAAATGTAATCGATGATGAGTTT 1243  
Db 1207 CGACAGGATTAAGGTGTGTTTGGTTTAGAACAAGCTTTAATATTTGCAATTT 1261

RESULT 13  
US-10-185-578-1  
; Sequence 1, Application US/10185578  
; Patent No. 6974893  
; GENERAL INFORMATION:  
; APPLICANT: Shanklin, John  
; APPLICANT: White, Edward J.  
; TITLE OF INVENTION: Isoform of Castor Oleate Hydroxylase  
; FILE REFERENCE: DOW-07606  
; CURRENT APPLICATION NUMBER: US/10/185,578  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/302,801  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1164  
; TYPE: DNA  
; ORGANISM: Ricinus communis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1164)  
; OTHER INFORMATION:  
US-10-185-578-1

Query Match 29.7%; Score 417.2; DB 4; Length 1164;

Best Local Similarity 62.1%; Pred. No. 1.1e-104;  
Matches 678; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

QY 138 AACGAGCCCGGATTTGATCGGGCCCATCTCTGTTAAGTGATCTTAAAGAAAGCAATCCCTG 197  
DB 77 AGGAGCGCGGACACGAAGCCCTCTTACACTTGTGACCTCAAGAGGCCATCCAC 136

QY 198 CACATTGCTTCGGCGGATCGCGCTGCTGTCATCTGTCAGTGTTCAGGATCTCATTA 257  
DB 137 CCATTGCTTTGAACGCTCTTTTGTGGCTCATCTCTTATGTCCTATGTCATGTCGTCT 196

QY 258 TCACCTTCCTTTTATACAGGTGCGCAACACCTTACATTCCTCCTCCTCCCTCTAG 317  
DB 197 TAAGTTTCTTTCTACTCGATCGCCCAACTTCTTCCCTTACATCTCTTCTCCGCTCT 256

QY 318 TTTACTTAGCATCGCGGTTTACTGTTTGGCAATCTTGCACTCTCCTCCTGTTTATGG 377  
DB 257 CGTATGTCGTTGGCTGTTTACTGCTCTTCCAGGCTGCACTTCACTGCTGTTGG 316

QY 378 TCCTCGGCATGAATCGGCCATCATGCTTCTAGTACGACCTGATGATGATGATGATG 437  
DB 317 TCATCGGCATGAATGCGCATCATGCTTTTGTAGTATGATGATGATGATGATGATG 376

QY 438 TTGGATTGCTTCCATTCGGCTCTCTCCTCCTCCTTACTTTTCTGGAATACAGCATC 497  
DB 377 TTGGCCTAATTTGCTAATTCGCACTTCTGCTTCCATATTTTTCATGGAATATAGCATC 436

QY 498 GAAAGCACCATGCAACACAAATTTACTCGAAACGAGGAAGTTTACATTCCTPAGAATC 557  
DB 437 GCGGCACCACTTCAACATAGGATCTCTGAGGAGACGAGTGTGCTCCGGAATCAA 496

QY 558 AGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACACACGCTGTCGAATCC 617  
DB 497 AGTCGAAATTTTCATGTTTCTTAAGTAC-----TTAAACAACCCGCGAGTTCGAGTTT 550

QY 618 TCATCTTGTCATCATGTTAACTTAGGATTTCTTTATACCTCTTAAAGATTTTTCAG 677  
DB 551 TGACACTTGTGTCAGGCTCTCTTGTGCTGGCTTTTATACCTTTAGCTTTCAATGTCTCTG 610

QY 678 GCAGAAGTACGATAGATTTACCAACCACTTTCATGCTGAGCCGATCTTCCACGAGC 737  
DB 611 GTAGACCTTACGATCGCTTGTGTCATATGATCTTATGCTTATGCTTATGCTTATGCTG 670

QY 738 GTGAGCGAATCCAGGTTGCGTTATCAGATCTGCTGATCGTTGAGTGTTTTACGACTCA 797  
DB 671 GAGAAGGCTTCAGATTACATTGCTGACCTCGAATCTTTGCCACAACGTTTGTGCTT 730

QY 798 AGTTTCTGTACAAAACAAAGGATTTGTTGGTGATGTCATGATGAGGATTCAGTGA 857  
DB 731 ATCAGGCTACAAATGGCAAAAGGTTGGCTTGGGTAATGCGTATCTATGGGTCGCTATGC 790

QY 858 TAGGTCGTAATCTCTTCAATTCGTAATCACTTATCTGACACACACATCTGCTGTCAC 917  
DB 791 TTAATGTTAACTGTTTCTTCTTGTATGATCACTATCTTGCAGACACTCACCCAGCTATTC 850

QY 918 CCAATTACGATTCACCGAATGAACTGGATCAAGAGGCTTTGACCAACATCGACAGAG 977  
DB 851 CAGCTATGCTCATCGAATGGATTTGGCTCGGGGAGCAATGGTCACTGTCATGATAGAG 910

QY 978 ATTTCCGCTCTCTGAAATCGGGTTTTTCCACGATTTTACACACCCAGTGTTCACCAAT 1037  
DB 911 ATTATGGGTGTTGAATAAAGTATTCATAAATTCAGACACTCATGTAGCTCATCATC 970

QY 1038 TGTTTCCCTACATTCACATTCATGCAAGAGGCGAGGCGGATCAAGCCATCT 1097  
DB 971 TCTTTGCTACAGTGCCACATTCATGCAATGAGGCGCACTAAGCAATCAAGCCTATAA 1030

QY 1098 TGGGTGATTTACAGGATGATCGACAGGACTCTCATTTTCAAGCAATGTGGAGAGAGCCA 1157  
DB 1031 TGGGTGATTTACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1090

QY 1158 AGGAATGCAATTTATCATCGAAGCAAGATGACAGACGACGACCAAGAGGACATATTTGGTACC 1217

DB 1091 AGGAGTGTGTTGTCGAGCCAGATGAAGGAGTCTCTACACAAGCGGTTTCTGTGTTACC 1150

QY 1218 ATAAATGTAAAT 1229  
DB 1151 GGAACAAGTATT 1162

RESULT 14  
US-08-314-596-43  
; Sequence 43, Application US/08314596  
; Patent No. 5668292  
; GENERAL INFORMATION:  
; APPLICANT: SOMERVILLE, CHRIS  
; APPLICANT: VAN DE LOO, FRANK  
; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN L.L.P.  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/314,596  
; FILING DATE: 26-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 206905/1220  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1222 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-314-596-43

Query Match 29.7%; Score 417.2; DB 2; Length 1222;  
Best Local Similarity 62.1%; Pred. No. 1.2e-104;  
Matches 678; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

QY 138 AACGAGCCCGGATTTGATCGGGCCCATCTCTGTTAAGTGATCTTAAAGAAAGCAATCCCTG 197  
DB 37 AGGAGCGCGGACACGAAGCCCTCTTTCACACTTGTGACCTCAAGAGAGCCATCCAC 96

QY 198 CACATTGCTTCGGCGGATCGCGCTGCTGTCATCTGCTAGCTAGTGTTCAGGATCTCATTA 257  
DB 97 CCATTGCTTTGAGACCTCTTTTGTGGCTCATCTTCCCTATGTTGCTATGATGCTGCT 156

QY 258 TCACCTTCCTTTTATACAGGTGCGCAACACCTTACATTCCTCACCTCCCTCCCTCTAG 317  
DB 157 TAAGTTTCTTTTCTACTCGATCGCCACCAACTTCTTCCCTTACATCTCTTCTCCGCTCT 216

QY 318 TTTACTTAGCATCGCGGTTTACTGTTTGGCAATCTTGCATCTCCTCCTGTTTATGG 377  
DB 217 CGTATGTCGTTGGCTGTTTACTGCTCTTCCAGGCTGCACTTCTCACTGCTTTGG 276

QY 378 TCCTCGGCATGAATCGCGCCATCATGCTTTTAGTGAGTACCAAGTGGATTTGATAAGCCG 437  
DB 277 TCATCGGCCATGAATGCGCCATCATGCTTTTAGTGAGTATCAGCTGGCTGATGACATTG 336

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QY 438 TTGGATTGCTCTGCTCAATTCGGCTCTCCTCACCCCTTACTTTCTTGGAAATACAGCCATC 497
DB 337 TTGGCTTAATTTGCTCAATTCGCACTTCTGGTTCATATTTTTCATGGAATATAGCCATC 396
QY 498 GAAAGCACCATCGCAACACAAATTCACTCGAAACGAGAGAGTTTACATCTCTAGAACTC 557
DB 397 GCCGCCACATCTTAACATAGATCTCTCGACGAGAGAGAGTGTCTGTCGGAATCAA 456
QY 558 AGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGAACAACGCTGCTGGTGAATCC 617
DB 457 AGTCGAAATTTCAATGATTTCTAGTACTCA-----AACACCCGCCAGCTCGAGTTT 510
QY 618 TCATCTTGGTCATCATGTTAACCTTAGATTTCTCTTTTATACCTCTTAACGAATGTTTCAG 677
DB 511 TGACACTTGTGCGCACGCTCTCTCTGCTGGCTTGTATCTTACTTGTCAATGTCCTG 570
QY 678 GCAAGAGTACGATAGATTTTACCAACCACTTTGATGCCATTTGATGCCATTTTACCGGAGC 737
DB 571 GTAGACCTTACGATCGCTTGTGCTGCAATATGATCCCTATGCGCCATATTTCCGAA 630
QY 738 GTAGCGAATCAGGCTTGGTTATCAGATCTTGGTATCGTTGCACTGTTTACGAGCTCA 797
DB 631 GAGAAAGGCTTCAGATTTACATTTGCTGACCTCGGAATCTTTGCCACAACGTTTGTGCTT 690
QY 798 AGTTCTTGTACAAACAAAGATTTGGTTGGTGATGTGATGATGATGATGATGATGATGAT 857
DB 691 ATCAGGCTACAAATGCAAAAGGTTGGCTTGGGTAATGCTATCTATGGGGTGCCATTC 750
QY 858 TAGGTCTGAATTCCTTATTCATTAATCGTAATCACCTTATCTGCACACACACATCTGTCGTCAC 917
DB 751 TTATTTGTAATCTGTTCTTCTGTTATGATCATACTTGCAGCACACTCACCCAGCTATTC 810
QY 918 CCCATTACGATTTCAACCGAATGGAATCGAATCAAAAGGAGCCTTGACCAATTCGACAGAG 977
DB 811 CACGCTATGGCTCATCGGAATGGGATTTGGCTCCGGGGAGCAATGGTGACTGTGATAGAG 870
QY 978 ATTTGGGCTCTGTAATCGGTTTCCAGGAGTTTACACACACCCAGCTTGTGACCAATTT 1037
DB 871 ATTATGGGGTGTGAATAAAGTATTTCCATAATTTGCAGACACTCATGTAGCTCATCATC 930
QY 1038 TGTTTTCCCTACATTCACATATATGCAAAAGGAGCAAGCGAGGCCATCAAGCCAAATCT 1097
DB 931 TCTTTGCTACAGTGCCACATTAACCATGATGATGATGATGATGATGATGATGATGATGAT 990
QY 1098 TGGGTGATTTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATGTGGAGAGGCCA 1157
DB 991 TGGGTGATTTATACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1050
QY 1158 AGGAATGCATTTACATCGAGCAAGATGCGACAGCAGCAAGCAAGGAGCATATTTGTTACC 1217
DB 1051 AGGAGTGTCTTGTCTCGAGCCAGATGAAGGAGCTCTCTACACAAAGGCGGTTTCTGGTACC 1110
QY 1218 ATAAAAATGTAAT 1229
DB 1111 GGAACAAGTATT 1122
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RESULT 15
US-08-320-982-43
; Sequence 43, Application US/08320982
; Patent No. 5801026
; GENERAL INFORMATION:
; APPLICANT: SOMERVILLE, CHRIS
; APPLICANT: VAN DE LOO, FRANK
; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
; PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
```

```
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,982
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,596
; FILING DATE: 26-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 206905/1220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1222 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-320-982-43
```

```
Query Match 29.7%; Score 417.2; DB 2; Length 1222;
Best Local Similarity 62.1%; Pred. No. 1.2e-104;
Matches 678; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

QY 138 AACGAGCCCGGATTCATCCGGCGCATTCCTCGTTAAGTGATCTAAAGAAAGCAATCCCTG 197
DB 37 AGCGAGCGCGCACACGAAAGCTCTCTTTCACACTTGGTGACCTCAAGAGAGCATCCCATC 96
QY 198 CACATTGCTTCGGCGGATTCGGTTCATCTGCTAGCTAGTTCAGATCTCATTA 257
DB 97 CCCATTGCTTTGAACGCTCTTTTGTGGCTCAITTCCTCTATGTTGCTCTGCTCTGCT 156
QY 258 TCACCTCTCTTTTATACACGGTCGCAACACACTACATATCTCCTCACCTCCTCCTCTAG 317
DB 157 TAAGTTTCTTTTCTACCTGATCGCCACCACTTCTTCCCTTACATCTCTTCTCGCTCT 216
QY 318 TTTACTTAGCATGCGCGGTTTACTGTTTTCGCAATTTGCACTCTCACTGCTTATGGG 377
DB 217 CGTATGCTGCTTGGCTGTTTACTTGGCTCTTCCAAGGCTGCATCTCACTGCTCTTGGG 276
QY 378 TCCTCGGCGCATGATCGCGGCATCATGCTTTAGTGAGTACAGTGGATTCATACGCGG 437
DB 277 TCATCGGCGCATGATGTCGCCATCATGCTTTTAGTGAGTATCAGCTGCTGATGACATTG 336
QY 438 TTGGATTGCTCTCCATTCGGCTCTCCTCACCCCTTACTTTTCTTGGAAATACAGCCATC 497
DB 337 TTGGCTTAATTTGCTCAATTCGCACTTCTGCTTCCATATTTTTCATGGAATATAGCCATC 396
QY 498 GAAAGCACCATCGCAACACAAATTCACTCGAAACGAGAGAGTTTACATCTCTAGAACTC 557
DB 397 GCCGCCACCAATCTAAACATAGGATCTCTCGACGAGAGAGAGTGTCTGTCGGAATCAA 456
QY 558 AGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGAACAACGCTGCTGGTGAATCC 617
DB 457 AGTCGAAATTTCAATGATTTCTAGTACTCA-----AACACCCGCCAGCTCGAGTTT 510
QY 618 TCATCTTGGTCATCATGTTAACCTTAGATTTCTCTTTTATACCTCTTAACGAATGTTTCAG 677
DB 511 TGACACTTGTGCGCACGCTCTCTCTGCTGGCTTGTATCTTACTTGTCAATGTCCTG 570
QY 678 GCAAGAGTACGATAGATTTTACCAACCACTTTGATGCCATTTGATGCCATTTTACCGGAGC 737
DB 571 GTAGACCTTACGATGCTTGTGCTGCAATATGATCCCTATGCGCCATATTTCCGAA 630
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|    |      |   |      |
|----|------|---|------|
| QY | 738  | GTGAGCGAATCCAGGTGGCTTATCAGATCTTGGTATCGTTGCGAGTGTCTTACGGACTCA  | 797  |
| Db | 631  | GAGAAAGGCTTCAGATTTACATTTGCTGACCTCGGAATCTTTGCCACAACGTTTGTGCTTT | 690  |
| QY | 798  | AGTTTCTTGTACAAACAAAGGATTTGGTGGTGATGTGCATGTATGGAGTTCAGTCA      | 857  |
| Db | 691  | ATCAGGCTACATGGCAAAAGGTTGGCTTGGGTAATGCGTATCTATGGGGTGCCATTGC    | 750  |
| QY | 858  | TAGTCTGAATTCCTTCATTTATCGTAAATCACTTATCTGCACCACACACATCTGTCTCAC  | 917  |
| Db | 751  | TTATTGTTAACTGTTTCCTTGTATGATCACATCTTGCAGCACACTCACCCAGCTATTTC   | 810  |
| QY | 918  | CCCAITACGATTCAACCGAATGGAACTGGATCAAGAGCCTTGAACCAATCGACAGAG     | 977  |
| Db | 811  | CACGCTATGGCTCATCGGAATGGGATTTGGCTCCGGGGAGCAATGGTCACTGTGATAGAG  | 870  |
| QY | 978  | ATTTCCGTCTCCTGAATCGGTTTTCACGACGTTACACACACCCACGTTGTCACCAT      | 1037 |
| Db | 871  | ATTATGGGGTGTGAATAAGTATTCATAACATTCGACACACTCATGTAGCTCATCATC     | 930  |
| QY | 1038 | TGTTTCCCTACATTCACACATTTATGCAAAAGGAGGCAAGCGAGGCCATCAAGCCAATCT  | 1097 |
| Db | 931  | TCCTTCTACAGTGCCACATTTACCATGCAATGGAGGCCACTAAGCAATCAGCCTATAA    | 990  |
| QY | 1098 | TGGTGATTACAGGATGATCGACAGACTCCCATTTTTCAAAGCAATGTGGAGAGGCCA     | 1157 |
| Db | 991  | TGGGTGAGTATTACCGGTATGATGGTACCCCATTTTACAAGGCATTTGTGGAGGGGCAA   | 1050 |
| QY | 1158 | AGGAATGCCATTTACATCGAGCAAGATGCAGACAGCAAGCAAGGAGACATATTGGTACC   | 1217 |
| Db | 1051 | AGGAGTGTCTTGTCTCGAGCCAGATGAAGGAGCTCCTACACAAGGCGTTTCTGTGTACC   | 1110 |
| QY | 1218 | ATAAAATGTAAT  | 1229 |
| Db | 1111 | GGACAAATATT   | 1122 |

Search completed: September 25, 2006, 01:08:35  
Job time : 298 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2006, 22:33:01; Search time 1361 Seconds  
(without alignments)  
7202.778 Million cell updates/sec

Title: US-10-622-774-1  
Perfect score: 1406  
Sequence: 1 gtaggtttgggtgcggtg.....aaaaaaaaaaaaaaaaaaaaa 1406

Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N\_Geneseq\_8.\*
- 1: Geneseqn1980s.\*
  - 2: Geneseqn1990s.\*
  - 3: Geneseqn2000s.\*
  - 4: Geneseqn2001as.\*
  - 5: Geneseqn2001bs.\*
  - 6: Geneseqn2002as.\*
  - 7: Geneseqn2002bs.\*
  - 8: Geneseqn2003as.\*
  - 9: Geneseqn2003bs.\*
  - 10: Geneseqn2003cs.\*
  - 11: Geneseqn2003ds.\*
  - 12: Geneseqn2004as.\*
  - 13: Geneseqn2004bs.\*
  - 14: Geneseqn2005s.\*
  - 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 1406  | 100.0       | 1406   | 14 | ADW68586 | Adw68586 Stokesia  |
| 2          | 870   | 61.9        | 1364   | 2  | AAV72550 | Aav72550 Vernonia  |
| 3          | 870   | 61.9        | 1364   | 14 | ADW68594 | Adw68594 Vernonia  |
| 4          | 697   | 49.6        | 1137   | 14 | AEC02364 | Aec02364 Stokesia  |
| 5          | 681.6 | 48.5        | 1134   | 13 | ADR87346 | Adr87346 Hydroxyly |
| 6          | 681.6 | 48.5        | 1134   | 14 | AEC02260 | Aec02260 Stokesia  |
| 7          | 673   | 47.9        | 1285   | 4  | AAF88311 | Aaf88311 C. offic  |
| 8          | 665.6 | 47.3        | 1134   | 13 | ADR87352 | Adr87352 Codon opt |
| 9          | 665.6 | 47.3        | 1134   | 14 | AEC02266 | Aec02266 Stokesia  |
| 10         | 657.8 | 46.8        | 1125   | 13 | ADR87325 | Adr87325 Hydroxyly |
| 11         | 657.8 | 46.8        | 1125   | 14 | AEC02239 | Aec02239 Crepis bi |
| 12         | 657.6 | 46.8        | 1312   | 2  | AAV63102 | Aav63102 Crepis sp |
| 13         | 646   | 45.9        | 1143   | 13 | ADR87331 | Adr87331 PAD2/Hydr |
| 14         | 640.4 | 45.5        | 1143   | 14 | AEC02245 | Aec02245 Crepis bi |
| 15         | 640.4 | 45.5        | 1344   | 14 | ADW68595 | Adw68595 Crepis pa |
| 16         | 640.4 | 45.5        | 1358   | 2  | AAV63101 | Aav63101 Crepis pa |
| 17         | 640.4 | 45.5        | 1358   | 14 | ADX69238 | Adx69238 Delta-12  |
| 18         | 640.4 | 45.5        | 1358   | 14 | ADX85617 | Adx85617 DNA encod |

|    |       |      |      |    |          |                    |
|----|-------|------|------|----|----------|--------------------|
| 19 | 640.4 | 45.5 | 1358 | 14 | ADW88813 | Adw88813 C. palae  |
| 20 | 638.6 | 45.4 | 1125 | 13 | ADR87351 | Adr87351 Codon opt |
| 21 | 638.6 | 45.4 | 1125 | 14 | AEC02265 | Aec02265 Crepis bi |
| 22 | 612.8 | 43.6 | 1435 | 14 | ADX18009 | Adx18009 DNA encod |
| 23 | 612.8 | 43.6 | 1435 | 14 | ADX69236 | Adx69236 Delta-12  |
| 24 | 612.8 | 43.6 | 1435 | 14 | ADX85615 | Adx85615 DNA encod |
| 25 | 611.2 | 43.5 | 1128 | 2  | AAT95688 | Aat95688 Crepis al |
| 26 | 486.4 | 34.6 | 1134 | 13 | ADR87348 | Adr87348 Codon opt |
| 27 | 486.4 | 34.6 | 1134 | 14 | AEC02262 | Aec02262 Stokesia  |
| 28 | 470.6 | 33.5 | 1125 | 14 | AEC02365 | Aec02365 Crepis bi |
| 29 | 467.2 | 33.2 | 1125 | 14 | AEC02363 | Aec02363 Crepis pa |
| 30 | 467   | 33.2 | 6220 | 12 | ADH51189 | Adh51189 Soybean F |
| 31 | 467   | 33.2 | 6220 | 12 | ADI03850 | Adi03850 Soybean F |
| 32 | 462.6 | 32.9 | 1586 | 13 | ADX31958 | Adx31958 Plant ful |
| 33 | 459.8 | 32.7 | 1457 | 13 | ADX29962 | Adx29962 Plant ful |
| 34 | 440.4 | 31.3 | 1640 | 10 | ADF55608 | Adf55608 Spinach f |
| 35 | 430.6 | 30.6 | 1152 | 13 | ADR87326 | Adr87326 PAD2/Hydr |
| 36 | 430.6 | 30.6 | 1152 | 14 | AEC02240 | Aec02240 Castor be |
| 37 | 430.6 | 30.6 | 1541 | 13 | ADR60394 | Adr60394 Cotton CD |
| 38 | 426.2 | 30.3 | 1369 | 6  | ABL58599 | AbL58599 Cress mic |
| 39 | 426.2 | 30.3 | 1372 | 2  | AAQ66068 | Aaq66068 Sequence  |
| 40 | 426.2 | 30.3 | 1372 | 3  | AAZ51315 | Aaz51315 A. thalia |
| 41 | 426.2 | 30.3 | 1372 | 14 | ADY79693 | Ady79693 Arabidops |
| 42 | 426.2 | 30.3 | 1615 | 14 | AEBA8230 | Aeb48230 Nucleotid |
| 43 | 426.2 | 30.3 | 1619 | 13 | ADR89457 | Adr89457 PAD2 desa |
| 44 | 424.6 | 30.2 | 1451 | 3  | AAC39493 | Aac39493 Arabidops |
| 45 | 424.6 | 30.2 | 2973 | 2  | AAQ66074 | Aaq66074 Sequence  |

ALIGNMENTS

RESULT 1

ADW68586  
ID ADW68586 standard; cDNA; 1406 BP.

AC ADW68586;

DT 07-APR-2005 (first entry)

DE Stokesia laevis fatty acid epoxigenase cDNA.

XX DNA purification; transgenic plant; plant; expression; recombinant DNA;

KW seed oil; soybean oil; linseed oil; plastic;

KW delta 12-fatty acid epoxigenase; delta 12-epoxigenase;

KW delta 12-epoxidase; gene; ds; transgene.

XX Stokesia laevis.

OS Stokesia laevis.

FH Key Location/Qualifiers

FT CDS 92..1228

FT /\*tag= a

FT /product= "Stokesia laevis fatty acid epoxigenase"

XX US2005022270-A1.

XX 27-JAN-2005.

XX 21-JUL-2003; 2003US-00622774.

XX 21-JUL-2003; 2003US-00622774.

XX (HILD/) HILDEBRAND D.

XX (HATA/) HATANAKA T.

XX Hildebrand D, Hatanaka T;

XX WPI; 2005-111979/12.

XX P-PSDB; ADW68587.

XX New isolated nucleic acid molecule encoding a delta 12-fatty acid  
PT epoxigenase enzyme, useful for genetically producing industrial products  
PT including coating, composites, adhesives and plasticizers.

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XX PS Claim 5; SEQ ID NO 1; 22pp; English.
XX CC The present invention relates to a nucleic acid molecule encoding a delta
CC 12-fatty acid epoxidase enzyme. The invention is useful for genetically
CC producing raw materials in the manufacture of industrial products
CC including coating, composites, adhesives and plasticizers. The present
CC sequence is the Stokesia laevis fatty acid epoxidase cDNA.
XX SQ Sequence 1406 BP; 403 A; 322 C; 289 G; 392 T; 0 U; 0 Other;

Query Match 100.0%; Score 1406; DB 14; Length 1406;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGGTTTGGGTCGGTGAGATCAGTGTTCGACCGAAATCCAAACGCAATTTCTAAATTT 60
Db 1 GTAGGTTTGGGTCGGTGAGATCAGTGTTCGACCGAAATCCAAACGCAATTTCTAAATTT 60

Qy 61 GGATTTTCAAAATCTGGGAGAGGTAGCAGATGTCCGATTCATATGATGATCGAATGAA 120
Db 61 GGATTTTCAAAATCTGGGAGAGGTAGCAGATGTCCGATTCATATGATGATCGAATGAA 120

Qy 121 AGATCATGATATGACGACGAGCCCGATTTGATCCGCGCCATTTCTCGTTAAGTGATCT 180
Db 121 AGATCATGATATGACGACGAGCCCGATTTGATCCGCGCCATTTCTCGTTAAGTGATCT 180

Qy 181 AAGAAAGCAATCCCTGCACATTTGTTCCGGCGATTCGCGCGTCTGGTTCATCTCTGCTAGT 240
Db 181 AAGAAAGCAATCCCTGCACATTTGTTCCGGCGATTCGCGCGTCTGGTTCATCTCTGCTAGT 240

Qy 241 AGTTCAGGATCTCATATATACGCTTCTTTTATACACGTCGCGACACCTACATCTCTCA 300
Db 241 AGTTCAGGATCTCATATATACGCTTCTTTTATACACGTCGCGACACCTACATCTCTCA 300

Qy 301 CCTCCTCCTCCTCTAGTTTACTTAGCATGCGCGTCTTACTGGTTTGGCCAACTCTTGCA 360
Db 301 CCTCCTCCTCCTCTAGTTTACTTAGCATGCGCGTCTTACTGGTTTGGCCAACTCTTGCA 360

Qy 361 CCTCAGTGGTTTATGGTTCCTCGGCATGAATGCGGCGCATGCTCTTCTAGTGATACCA 420
Db 361 CCTCAGTGGTTTATGGTTCCTCGGCATGAATGCGGCGCATGCTCTTCTAGTGATACCA 420

Qy 421 GTGATTTGATTAACGCGTTGATTTGCTCCTCATTTGGCTCTCTCACCCTTACTTTTC 480
Db 421 GTGATTTGATTAACGCGTTGATTTGCTCCTCATTTGGCTCTCTCACCCTTACTTTTC 480

Qy 481 TTGGAATATACAGCCATCGAAAGCACCATGCAAAACAAATTCACCTCGAAACGAGGAAT 540
Db 481 TTGGAATATACAGCCATCGAAAGCACCATGCAAAACAAATTCACCTCGAAACGAGGAAT 540

Qy 541 TTACATTCCTAGAACTCAGTCCAGCTCAGGATTTACTCCACATACGAAATTTCTTGCAA 600
Db 541 TTACATTCCTAGAACTCAGTCCAGCTCAGGATTTACTCCACATACGAAATTTCTTGCAA 600

Qy 601 CACGCTGGTGAATCTCTATCTGGTCAATCATGTTTAACTTACCTTAGATTTCTTTATACCT 660
Db 601 CACGCTGGTGAATCTCTATCTGGTCAATCATGTTTAACTTACCTTAGATTTCTTTATACCT 660

Qy 661 CTTTACGAAATGTTTTCAGGCAAGAAGTACGATGATTTTACCAACCACTTTTGATTCGAG 720
Db 661 CTTTACGAAATGTTTTCAGGCAAGAAGTACGATGATTTTACCAACCACTTTTGATTCGAG 720

Qy 721 CCCGATCTTCCAGCGGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGC 780
Db 721 CCCGATCTTCCAGCGGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGC 780

Qy 781 AGTGTGTTTACGACATCAAGTTCTTGTACAAACAAAGGATTTGGTGGGTGATGTCAT 840
Db 781 AGTGTGTTTACGACATCAAGTTCTTGTACAAACAAAGGATTTGGTGGGTGATGTCAT 840

Qy 841 GTATGAGGTTCCAGTGATAGGTCGAATTCCTTCAATTCATTAATCGTAATCTATCTGCACCA 900

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Db 841 GTATGAGGTTCCAGTGATAGGTCGAATTCCTTCAATTCATTAATCGTAATCTATCTGCACCA 900
Qy 901 CACACATCTGCTGTACCCCAATTAAGATTCAACCGAATGGAATCGATCAAGAGGCTT 960
Db 901 CACACATCTGCTGTACCCCAATTAAGATTCAACCGAATGGAATCGATCAAGAGGCTT 960
Qy 961 GACCAATTCGACGAGATTTCCGTCCTCCGAAATCGGTTTCCACGACGTTACACAC 1020
Db 961 GACCAATTCGACGAGATTTCCGTCCTCCGAAATCGGTTTCCACGACGTTACACAC 1020

Qy 1021 CCACGTTTGCACCAATTTGTTTCCCTACATTCACATTTATCATGCAAGGAGCAAGCGA 1080
Db 1021 CCACGTTTGCACCAATTTGTTTCCCTACATTCACATTTATCATGCAAGGAGCAAGCGA 1080
Qy 1081 GGCCATCAAGCCCAATCTTGGGTGATTTACAGGATGATCGACGAGCTCCATTTTCAAAGC 1140
Db 1081 GGCCATCAAGCCCAATCTTGGGTGATTTACAGGATGATCGACGAGCTCCATTTTCAAAGC 1140

Qy 1141 AATGTGGAGAGGCGCAAGGAATGCAATTTACATCGAGCAAGATGACAGACGAGCAACAA 1200
Db 1141 AATGTGGAGAGGCGCAAGGAATGCAATTTACATCGAGCAAGATGACAGACGAGCAACAA 1200
Qy 1201 AGGACATATTTGGTACCATTAATGTAATCGATGAGGTTTGTAGTTGGAATTAATGACA 1260
Db 1201 AGGACATATTTGGTACCATTAATGTAATCGATGAGGTTTGTAGTTGGAATTAATGACA 1260

Qy 1261 TGACGATCCTTTTGTATGCTTGAATCGTTCTATTTCTTTTATATGTTTGTAGATAAA 1320
Db 1261 TGACGATCCTTTTGTATGCTTGAATCGTTCTATTTCTTTTATATGTTTGTAGATAAA 1320

Qy 1321 TAAGTAATCTTTGAGTGAAGATGGGAGGAGCAAGAAACAAAGCAATATAATACGCTAAAA 1380
Db 1321 TAAGTAATCTTTGAGTGAAGATGGGAGGAGCAAGAAACAAAGCAATATAATACGCTAAAA 1380

Qy 1381 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1406
Db 1381 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1406

RESULT 2
AAV72550
ID AAV72550 standard; cDNA; 1364 BP.
XX AC AAV72550;
XX DT 27-AUG-2003 (revised)
XX DT 10-FEB-1999 (first entry)
XX DE Vernonia galamenensis fatty acid epoxidising enzyme encoding cDNA.
XX KW Vernonia galamenensis; fatty acid desaturase; epoxidising enzyme;
XX OS Vernonia galamenensis.
XX PH Key Location/Qualifiers
XX FT CDS 103..1257
XX FT /*tag= a
XX PN US5846784-A.
XX PD 08-DEC-1998.
XX PF 11-JUN-1997; 97US-00872302.
XX PR 11-JUN-1997; 97US-00872302.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Hitz WD;
XX DR WPI; 1999-059065/05.
XX DR P-PSDB; AAW83354.

```

DNA encoding *Vernonia galamensis* fatty acid desaturase and fatty acid epoxidising enzyme - used to alter levels of expression of the enzymes in transformed host cells or to produce recombinant enzymes.

| Query Match           | 61.9%;  | Score 870;          | DB 2;           | Length 1364;      |
|-----------------------|---|---------------------|-----------------|-------------------|
| Best Local Similarity | 86.1%;  | Prod. No. 5.9e-206; |                 |                   |
| Matches 963;          | Conservative  | 0;                  | Mismatches 155; | Indels 0; Gaps 0; |
| 120                   | AAAGATCATGATATGACGAACGAGCCCGGATGATCCGGCGGCATTTCTCGTTAAAGTGATC   | 179                 |                 |                   |
| 149                   | ATGATCATATATATAACGACGTGCACCGTTGATCGGCGACCATTTCTCGTTAAGCGATC     | 208                 |                 |                   |
| 180                   | TAAAGAAAGCAATCCCTGCGACATTCCTTCGCGCGATCCGCGTCTGGTGCATCTCTGCTACG  | 239                 |                 |                   |
| 209                   | TAAAGAAAGCAATCCCTCGGCATTCGTTCCAGCGATCTGCCATCGGTTTCATCGTCTACG    | 268                 |                 |                   |
| 240                   | TAGTTTCAGGATCTCATATATACACTTCCTTTTATACACGTCGCGCAACACTTACATTCCTC  | 299                 |                 |                   |
| 269                   | TTGTTTCAGGATCTCATATATACCTTCCTTTTATACACGTCGCGCAACCTTACATTCCTC    | 328                 |                 |                   |
| 300                   | ACCTCCCTCCTCTCTAGTTTACTTAGCATGCGCGGTTTACTGGTTTTCGCCAATCTTGCA    | 359                 |                 |                   |
| 329                   | TTCTTCCTCCTCTCTACCTTACTTAGCATGGCTGTTTACTGGTTTTCGCCAATCTTGCA     | 388                 |                 |                   |
| 360                   | TCCTCACTGGTTTATGGGTCCTCGGCCATGAATCGGCCCATCATGCTTTTAGTGAGTACC    | 419                 |                 |                   |
| 389                   | TCCTCACTGGTTTATGGGTCATTTGGCCATGAATTTGGGCCATCATGCTTTATAGTGAGTACC | 448                 |                 |                   |
| 420                   | AGTGGATTGATAAACGCGGTTGGATTTCGTCCTCCATTTCGCTCTCTCTACCCCTTACTTTT  | 479                 |                 |                   |
| 449                   | AGTGGGTTGATAAACACCGTTTGGATTTCATCTCCATTCCTTTCTCTCAACCTTACTTTT    | 508                 |                 |                   |
| 480                   | CTTTGGAATATACAGCCATCGAAAGCACCATGCAAAACACAAATTCACTCGAAAACGAGGAG  | 539                 |                 |                   |
| 509                   | CTTTGGAATATACAGCCATCGAAAGCACCATGCGCAACACGAAATTCACTCGAAAACGAGGAG | 568                 |                 |                   |
| 540                   | TTTATACCTCTAGAACTCAGTCCGAGCTCAGGACTTACTCCACATACGAAATTTCTTGACA   | 599                 |                 |                   |
| 569                   | TTTATACCTCTAAAGCCAAAGTCCGAGCTCAGGAAATTACTCCAAATTTCAAATTTCTTGACA | 628                 |                 |                   |
| 600                   | ACACGCTGGTCGAATTCCTCATCTTGTGTCATCATGCTTAACCTTAGGATTTCTCTTTATACC | 659                 |                 |                   |
| 629                   | ACACCCCTGGTCGAATTCCTCATTTTGTCTTATCATGTTGACCTTGGGCTTTCTTTATACC   | 688                 |                 |                   |
| 660                   | TCCTTAACGAATGTTTTCAGCAAGAAAGTAGATAGATTTTACCAACCACTTTGATCCATTGA  | 719                 |                 |                   |
| 689                   | TCCTTGACCAATATTTTCAGSCAAGAAATACCAAGGTTTGGCCAAACCACTTTGATCCGTTGA | 748                 |                 |                   |
| 720                   | GGCCGATCTTACCGAGCGTAGCGGAATCCAGGTTGCGTTATTCAGATCTTGGTATCGTTG    | 779                 |                 |                   |
| 749                   | GGCCCATCTTTCAGTGAGCGGTGAACGAATCCAGGTCGTGCTATCCGATGTGGGTCTCAATG  | 808                 |                 |                   |
| 780                   | CAGTGTGTTTACCGACTCAAGTTTCTTGTGTACAAACAAAAGGATTTGGTTGGGTGATGTGCA | 839                 |                 |                   |
| 809                   | CTGTGTGTTTACGGGCTTAAGTTTCTTGTAGCGAAAAAAGGGTTTCGGTTGGGTAAATGCGCA | 868                 |                 |                   |
| 840                   | TGTATGGAGTTCAGTGATAGGTCTGAAATTCCTTCATTATCGTAATCACTTATCTGCACC    | 899                 |                 |                   |
| 869                   | TGTAACGAGCCCACTGGTTGGGCTGAATGCTCTCATTAATATGATCACTTATCTCCACC     | 928                 |                 |                   |

|                       |                   |   |                     |           |              |
|-----------------------|-------------------|---|---------------------|-----------|--------------|
| Query Match           |                   | 61.9%;  | Score 870;          | DB 14;    | Length 1364; |
| Best Local Similarity |                   | 86.1%;  | Pred. No. 5.9e-206; |           |              |
| Matches 963;          |                   | Conservative 0;   | Mismatches 155;     | Indels 0; | Gaps 0;      |
| Qy                    | 120               | AAGATCATGATGAGCAAGCGCCGATTTGATCCGGCGCCATCTCGTTAAAGTATC                    | 179                 |           |              |
| Db                    | 149               | ATGATCATATTAACGAAAGTGCACCGGTGTATGCGGCACCATTTCTGTTAAGCGATC                 | 208                 |           |              |
| Qy                    | 180               | TAAAGAAAGCAATCCCTGCACATTTGCTCCGGCGATCCGGCGATCTGTGTCATCCTGCTACG            | 239                 |           |              |
| Db                    | 209               | TAAAGAAAGCAATCCCTCGCATTTCTCCAGCGATCTGCCATCGTTTCATCGTCTACG                 | 268                 |           |              |
| Qy                    | 240               | TAGTTCAGGATCTCATATACCTTCTTTTATACACGGTCGCCAACACCTACATCTCTC                 | 299                 |           |              |
| Db                    | 269               | TTGTTTCAGGATCTCATATACCTTCTTTTATACACGGTCGCCAACCTCTTACATCTCTC               | 328                 |           |              |
| Qy                    | 300               | ACCTCCCTCCTCTAGTCTTACTTAGCATGGCGGTTTACTGTGTTTGCCAACTTTCGA                 | 359                 |           |              |
| Db                    | 329               | TTCTTCTCCTCCTCTACTTACTTAGCATGGCGGTTTACTGTGTTTGCCAACTTTCGA                 | 388                 |           |              |
| Qy                    | 360               | TCCTCAGTGGTTATGCGTCTCGGCCATGAATGCGGCATCATCGCTTTTAGTGAGTACC                | 419                 |           |              |
| Db                    | 389               | TCCTCAGTGGTTATGCGTCTCGGCCATGAATGCGGCATCATCGCTTTTAGTGAGTACC                | 448                 |           |              |
| Qy                    | 420               | AGTGAATGATAAGCCCGTTGGATTCGTCCTCCATTCGGCTCTCCTCACCCCTTACTTTT               | 479                 |           |              |
| Db                    | 449               | AGTGGGTTGATAACACCCGTTGGATTCATCTCTCCATTCCTTCTTCTCACACCTTACTTTT             | 508                 |           |              |
| Qy                    | 480               | CTTGGAAATACGCCATCGAAGACCAATGCAACACAAATTCATCTCGAAACGAGGAG                  | 539                 |           |              |
| Db                    | 509               | CTTGGAAATACGCCATCGAAGACCAATGCAACACAAATTCATCTCGAAACGAGGAGG                 | 568                 |           |              |
| Qy                    | 540               | TTTACATTTCTAGAACTCAGTCCCAAGCTCAGGACTTACTCCACATACGAATTTCTTGACA             | 599                 |           |              |
| Db                    | 569               | TTTACATTTCTAGAACTCAGTCCCAAGCTCAGGACTTACTCCACATACGAATTTCTTGACA             | 628                 |           |              |
| Qy                    | 600               | ACAGCCCTGGTGAATCTCTATTTGGTCATCATGTTAACTTAACTTAGGATTTCTCTTTATACC           | 659                 |           |              |
| Db                    | 629               | ACAGCCCTGGTGAATCTCTATTTGGTCATCATGTTAACTTAACTTAGGATTTCTCTTTATACC           | 688                 |           |              |
| Qy                    | 660               | TCTTAAACCAATGTTTCAGGCAAGATAGATAGATTTACCAACCACTTTGATCCATTTGA               | 719                 |           |              |
| Db                    | 689               | TCTTAAACCAATGTTTCAGGCAAGATAGATAGATTTACCAACCACTTTGATCCATTTGA               | 748                 |           |              |
| Qy                    | 720               | GCCGATCTTACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGATATCGTTG                | 779                 |           |              |
| Db                    | 749               | GCCGATCTTACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGATATCGTTG                | 808                 |           |              |
| Qy                    | 780               | CAGTGTTTTACGACTCAAGTTTCTTTGTACAAACAAAGGATTTGGTTGGGTGATGTGCA               | 839                 |           |              |
| Db                    | 809               | CTGTGTTTTACGGCTTAAGTTTCTTTGTAGCGAAAGGTTTCGGTTGGGTGATGTGCA                 | 868                 |           |              |
| Qy                    | 840               | TGTATGGAGTTCAGTGATAGTCTGAATTCCTTCAATTCGTATCACTTATCTGCACC                  | 899                 |           |              |
| Db                    | 869               | TGTACGGAGCCCGAGTGTGGGCTGGAATGCGCTTCATATATGATCATCTTATCTCCACC               | 928                 |           |              |
| Qy                    | 900               | ACACACATCTGTGCTCACCCATTAAGGATTCACCGAATGGAATCGGATCAAGAGGCT                 | 959                 |           |              |
| Db                    | 929               | ACACCCATCTGTCTCGCTCATTTAGGATTCGACCGAATGGATCGGATCAAGAGGCT                  | 988                 |           |              |
| Qy                    | 960               | TGACCAATACAGAGATTTGCTCTCTGAAATCGGGTTTTTCCACGAGTTACACACA                   | 1019                |           |              |
| Db                    | 989               | TGACTACAATCGATAGAGATTTGGTCTCTGAAATAGGTTTCCATGACGCTCACTACA                 | 1048                |           |              |
| Qy                    | 1020              | CCCAGTGTGACCACTTTGTTTCCCTCATCTCCATTCACATTCATCAAGAGGCGAAGC                 | 1079                |           |              |
| Db                    | 1049              | CACACGTGTGTCATTTGTTTCCCGTACATTTCCACATTTATCATCAAGAGGCGAAGC                 | 1108                |           |              |
| Qy                    | 1080              | AGGCCATCAAGCAATCTTGGGTGATTAACAGATGATCGACGAGTCTCATTTTTCAAAG                | 1139                |           |              |
| Db                    | 1109              | ACGCAATAAGCCGGTGTAGGGGATTCGATGATCGATGATCGATGATCGATGATCGATGAT              | 1168                |           |              |
| Qy                    | 1140              | CAATGTGGAGAGGCCCAAGNAATGCAATTTTACATCCGAGAGATGCAGACAGCAGCACA               | 1199                |           |              |
| Db                    | 1169              | CAATGTGGAGAGGCCCAAGNAATGCAATTTTACATCCGAGAGATGCAGACAGCAGCACA               | 1228                |           |              |
| Qy                    | 1200              | AAGGACATATTTGTTACCATATAAATTTGTAATCGATGATG                                 | 1237                |           |              |
| Db                    | 1229              | AAGGTGATATTTGTTACCATATAAATTTGTAATCGATGATG                                 | 1266                |           |              |
| RESULT 4              |                   |   |                     |           |              |
| AEC02364              |                   |   |                     |           |              |
| ID                    | AEC02364          | standard; cDNA; 1137 BP.  |                     |           |              |
| XX                    | AEC02364;         |   |                     |           |              |
| AC                    | AEC02364;         |   |                     |           |              |
| XX                    | 06-OCT-2005       | (first entry)   |                     |           |              |
| DT                    | 06-OCT-2005       | (first entry)   |                     |           |              |
| XX                    | Stokesia laevis   | epoxygenase encoding cDNA SEQ ID NO:131.                                  |                     |           |              |
| DE                    | Stokesia laevis   | epoxygenase; gene; ss.  |                     |           |              |
| XX                    | transgenic plant; | anthelmintic; epoxygenase; gene; ss.                                      |                     |           |              |
| KW                    | Stokesia laevis.  |   |                     |           |              |
| OS                    | Key               | Location/Qualifiers   |                     |           |              |
| XX                    | Key               | 1..1137   |                     |           |              |
| XX                    | CDS               | /*tag= a  |                     |           |              |
| FT                    | FT                | /product= "epoxygenase"   |                     |           |              |
| XX                    | XX                | US2005172358-A1.  |                     |           |              |
| PN                    | XX                | 04-AUG-2005.  |                     |           |              |
| XX                    | PD                | 04-AUG-2004; 2004US-00912534.   |                     |           |              |
| XX                    | XX                | 04-FEB-2004; 2004US-00772227.   |                     |           |              |
| XX                    | PR                | (VERB/) VERBSKY M L.  |                     |           |              |
| XX                    | PA                | (BAUB/) BAUBLITE C.   |                     |           |              |
| XX                    | PA                | (KLOE/) KLOEK A P.  |                     |           |              |
| XX                    | PA                | (DAVI/) DAVILA-APONTE J A.  |                     |           |              |
| XX                    | PA                | (HRES/) HRESKO M C.   |                     |           |              |
| XX                    | PA                | (MCLA/) MCLAIRD M B.  |                     |           |              |
| XX                    | PA                | (ZENT/) ZENTELLA R.   |                     |           |              |
| XX                    | PA                | (WILL/) WILLIAMS D J.   |                     |           |              |
| XX                    | Verbsky ML,       | Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;                        |                     |           |              |
| PI                    | McLaird MB,       | Zentella R, Williams DJ;  |                     |           |              |
| XX                    | XX                | WPI; 2005-603337/62.  |                     |           |              |
| DR                    | DR                | P-PSDB; AEC02369.   |                     |           |              |
| XX                    | XX                | New transgenic plant having a DNA construct comprising a nucleic acid     |                     |           |              |
| PT                    | PT                | encoding a protein for catalyzing the conversion of a substrate to a C16, |                     |           |              |
| PT                    | PT                | C18 or C20 monounsaturated fatty acid product, useful in preparing        |                     |           |              |
| PT                    | PT                | anthelmintic compounds.   |                     |           |              |
| XX                    | XX                | Claim 74; SEQ ID NO 131; 130pp; English.                                  |                     |           |              |
| PS                    | XX                | The invention relates to a transgenic plant containing at least one DNA   |                     |           |              |
| CC                    | CC                | construct comprising: (a) a nucleic acid encoding a polypeptide effective |                     |           |              |
| CC                    | CC                | for catalyzing the conversion of a substrate to a C16, C18, or C20        |                     |           |              |
| CC                    | CC                | monounsaturated fatty acid product; and (b) a regulatory element operably |                     |           |              |
| CC                    | CC                | linked to the nucleic acid encoding the polypeptide and conferring        |                     |           |              |
| CC                    | CC                | expression in a vegetative tissue of the plant. Also described: (1) a     |                     |           |              |
| CC                    | CC                | method of making a transgenic plant; (2) an isolated nucleic acid         |                     |           |              |
| CC                    | CC                | comprising the nucleotide sequence; (3) a recombinant nucleic acid        |                     |           |              |
| CC                    | CC                | construct comprising at least one regulatory element that confers         |                     |           |              |
| CC                    | CC                | expression in a vegetative tissue of a plant; and (4) a method of         |                     |           |              |
| CC                    | CC                | screening a transgenic plant for anthelmintic activity. The transgenic    |                     |           |              |
| CC                    | CC                | plant is useful in preparing compounds having anthelmintic activity. The  |                     |           |              |
| CC                    | CC                | present sequence encodes an epoxygenase which is used in the              |                     |           |              |
| CC                    | CC                | exemplification of the present invention.                                 |                     |           |              |

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|----|---|--|
| SQ | Sequence 1137 BP; 288 A; 228 C; 219 G; 402 T; 0 U; 0 Other;             |  |
|    | Query Match 49.6%; Score 697; DB 14; Length 1137;                       |  |
|    | Best Local Similarity 75.8%; Pred. No. 5.8e-163; Indels 0; Gaps 0;      |  |
|    | Matches 862; Conservative 0; Mismatches 275;                            |  |
| QY | 92 ATGTCGGATTCATATGATGATGAATGAAGATCATGATATGACGAAACGAGCCCGATTT 151       |  |
| DB | 1 ATGGCTTCCTCCTATGACGACGAATGAAGACCATGATATGGATGAAGAGCACCATA 60           |  |
| QY | 152 GATCCGGCGCCATTCCTGGTTAGTGATCTAAGAAAGCAATCCCTGCACATTCCTCCGG 211      |  |
| DB | 61 GACCCGCTGCTCTTCTCTCTCTGATCTTAAGAGGCTATCCAGCTCATTCGCTTTAGA 120        |  |
| QY | 212 CGATCCGCGCTCTGGTCATCCTCTAGTAGTTCAGGATCTCATATCACCTTCCTTTTA 271       |  |
| DB | 121 AGATCTGCTGTTGGTCTCTTCTGATCTTAAGAGGCTATTCAGACCTTATATTACTTTCCTTTG 180 |  |
| QY | 272 TACAGGTCGCGCAACACTACATTCCTCACCTCCCTCCTCTCTAGTTACTTTAGCATGG 331      |  |
| DB | 181 TATACCTGTGGCTAAACATTTATATCCACATCTTCCACCTCCACTTGTATCTTGTCTGG 240     |  |
| QY | 332 CCGGTTTACTGTTTGGCAATCTGCATCTCCTCACTGTTTATGGGTCTCGGCCATGAA 391       |  |
| DB | 241 CCAGTGATTTGGTTCGCCAATCTTGCAATCTTACGACTTTGGGTTCTTGGACATGAA 300       |  |
| QY | 392 TCGGGCCATCGCTCTTGTAGTGAGTACCACTGAGTGAAGCCCTTGATTCGTCTCCTC 451       |  |
| DB | 301 TCGGNACATCGCTTCTCTGATATCAATGATTCGACACGCTGTGGATTCGTCTT 360           |  |
| QY | 452 CATTCGGCTCTCCTCACCCCTTACTTTCTTGGAAATACAGCCATCGAAAGCACCATGCA 511     |  |
| DB | 361 CATTCGCTCTTTTGACTCCATATTTCTCTTGGAGTATTTCTCATAGAAGCATCATGCT 420      |  |
| QY | 512 AACACAAATCTACTCGAAACGAGGAGTTTACATTCCTAGAACTCAGTCCCGAGTCAGG 571      |  |
| DB | 421 AACACTAACTCTCTTGAGAACGAGGAGGTGTATTTCCAAGAACTCAATCTCAACTTGA 480      |  |
| QY | 572 ACTTACTCACAATACGAATTTCTTGACACAGCCCTGGTGAATCCTCATCTTGGTCATC 631      |  |
| DB | 481 ACTTATCTTACTATGAGTTCCTTGACAACTCCAGGAAGAAATCTTATCTTGTGATT 540        |  |
| QY | 632 ATGTTAACTTAGGATTTCTTTATACCTCTTTAAACGAATGTTTTCAGGCAAGATACGAT 691     |  |
| DB | 541 ATGCTTACTCTTGGATTTCCACTTTATCTTTTGACTAACGTGCTGGAAGAGTATGAC 600       |  |
| QY | 692 AGATTTACCAACCACTTTGATCATTTGAGCCGATCTTCACGAGCGTGAGGGAATCCAG 751      |  |
| DB | 601 AGATTCACATAACCAATTCGACCACCTTTCTCCAAATTTTCACTGAGAGAGAGAATCAA 660     |  |
| QY | 752 GTTGGGTTATCAGATCTTGATCGTTGAGTGTGTTTACGGACTCAAGTTTCTTGTAACA 811      |  |
| DB | 661 GTTGCTCTTTCTGATCTTGAATTTGGCTGTGTTCTATGGACTTAAGTTCTTGTTCAA 720       |  |
| QY | 812 ACAAGAGGATTTGGTTGGGTGATGTCATGTATGAGATTCAGTGTAGGTCTGAAATCC 871       |  |
| DB | 721 ACTAAGGATTTGGATGGGTATGTCATGTATGAGTGCAGTGTGCACTTAATCT 780            |  |
| QY | 872 TTCATTATCGTAAATCACTTATCTGACCAACACATCTGTGTCGCCCATACGATTCATCA 931     |  |
| DB | 781 TTCATTATTTGATTAATCTTATCTTATCATCACTCATCTTTCTTCTCCATTTATGATCT 840     |  |
| QY | 932 ACCGATGGAATCGGATCAAGAGGCTTGCACCAATCGACAGATTCCTGGTCTCCCTG 991        |  |
| DB | 841 ACTGAGTGAACCTGGATTAAGGTTGATTTGACTTATGACAGACTTCGGACTTTTG 900         |  |
| QY | 992 AATCGGGTTTTCACGACGTTACACACACCCAGTGTGACCAATTTGTTTCCCTACATT 1051      |  |
| DB | 901 AACAGAGTGTTCATGACGTGACTATCTATCTATCTGTCCTTCATCATCTTTCCCATATT 960     |  |
| QY | 1052 CCACATTATCATGCAAGAGGCAAGCGAGGCCATCAAGCCAACTTTGGGTGATTCAGG 1111     |  |
| DB | 961 CCACATTATCATGCTAAGGAGGCTTCTGAGGCTATTAAGCCAAATTTCTGGAGACTATAGA 1020  |  |

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|----|--|--|
| QY | 1112 ATGATCGACAGGACTCCATTTTCAAAGCAATGTGTGAGAGAGCCCAAGCAATGCATTAC 1171  |  |
| DB | 1021 ATGATTTAGTAGAATCCATTTTCAAGGCTATGTGTGAGAGAGGCTAAGGAGTGCATCTAT 1080 |  |
| QY | 1172 ATCGAGCAAGATGCGAGACAGCAAGGACAAAGGACATATTGGTACCATATAAATGTA 1228    |  |
| DB | 1081 ATTGAACAAGATGCTGACTCTAAGCATAGGGAACCTATTGGTATCATAGATGTAA 1137      |  |

|          |   |
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| RESULT 5 |   |
| ADR87346 |   |
| ID       | ADR87346 standard; cDNA; 1134 BP.   |
| XX       | AC ADR87346;  |
| XX       | AC ADR87346;  |
| DT       | 18-NOV-2004 (first entry)   |
| XX       | Hydroxylase/ epoxygenase coding sequence, SEQ ID 27.                      |
| DE       | Nematocide; Plant; 16C monounsaturated fatty acid;                        |
| XX       | 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;           |
| KW       | fatty acid epoxygenase; fatty hydroxylase; phospholipid:diacylglycerol;   |
| KW       | acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;            |
| KW       | hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;     |
| KW       | nematode; gene; ss.   |
| XX       | Stokesia laevis.  |
| OS       |   |
| XX       |   |
| XX       |   |
| FT       | Key   |
| FT       | CDS   |
| FT       | 1..1134   |
| FT       | /*tag= a  |
| XX       | /product= "Hydroxylase/ epoxygenase"                                      |
| PN       | WO2004071168-A2.  |
| XX       |   |
| PD       | 26-AUG-2004.  |
| XX       |   |
| PF       | 04-FEB-2004; 2004WO-US003254.   |
| XX       |   |
| PR       | 05-FEB-2003; 2003US-0445293P.   |
| XX       |   |
| PA       | (DIVE-) DIVERGENCE INC.   |
| XX       |   |
| PI       | Verbak ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;           |
| PI       | Hresko MC, McIaird MB, Zentella R;  |
| XX       |   |
| DR       | WPI; 2004-634973/61.  |
| DR       | P-PSDB; ADR87355.   |
| XX       |   |
| PT       | Novel transgenic plant containing DNA construct having nucleic acid       |
| PT       | encoding polypeptide for catalyzing conversion of substrate to            |
| PT       | monounsaturated fatty acid product, useful for controlling nematodes.     |
| XX       |   |
| PS       | Claim 74; SEQ ID NO 27; 180pp; English.                                   |
| XX       |   |
| XX       | The present invention relates to transgenic plants (I) containing one or  |
| CC       | more DNA constructs. The DNA constructs have a nucleic acid encoding a    |
| CC       | protein effective for catalyzing the conversion of a substrate to a 16C,  |
| CC       | 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid          |
| CC       | epoxygenase or a fatty hydroxylase, and a regulatory element operably     |
| CC       | linked to the nucleic acid encoding the protein, where the regulatory     |
| CC       | element confers expression in vegetative tissue of the plant. The fatty   |
| CC       | acid epoxygenase or a fatty hydroxylase can be                            |
| CC       | phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol      |
| CC       | acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty     |
| CC       | acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in |
| CC       | a vegetative tissue. The DNA construct of (I) is useful in the production |
| CC       | of hydroxylases and epoxygenases that controls nematode damage in         |
| CC       | commercially important plant species and so (I) exhibits increased        |
| CC       | resistance to nematodes. (I) provides an effective, environmentally safe  |
| CC       | methods of inhibiting nematode metabolism, growth, viability,             |
| CC       | development, infectivity and/or the nematode life cycle. (I) provides     |





CC exemplification of the present invention.

SQ Sequence 1134 BP; 297 A; 268 C; 229 G; 340 T; 0 U; 0 Other;

Query Match 48.5%; Score 681.6; DB 14; Length 1134;

Best Local Similarity 78.0%; Pred. No. 3.9e-159;

Matches 835; Conservative 0; Mismatches 229; Indels 6; Gaps 1;

QY 159 CGCATCTTCGTTAAGTGATCTAAAGAAAGCAATCCCTGCACATTCCTTCCGCGCATCG 218  
DB 71 CACCTTTCACATTAAGTGATATAAAGAAAGCAATCCCTCCCATTGCTTCAACAGATCG 130  
QY 219 CGCTCTGGTCATCCTGCTAGTGTTCAGATCTCATATATCATCTTCCCTTTTATACACGG 278  
DB 131 TCATACGTTTCGTCTACTATGTGTTCATGATCTCATCGTCTCTCATCGTCTTCTTCTTC 190  
QY 279 TCGCCAACCTACATCTCTCACTCCCTCCCTCTAGTTTACTTTAGCATGGCCGGTTT 338  
DB 191 TCGCAACGACATATATTAATGTTCTTCTGCTCTCTTGTCTTACATAGCGTGGCCAGTTT 250  
QY 339 ACTGGTTCCTCAATCTTGATCTCTCACTGGTTCCTGCGGCATGAATGCGGC 398  
DB 251 ACTGGTTCCTCAATCTTGATCTCTCACTGGTTCCTGCGGCATGAATGCGGC 310  
QY 399 ATCATGCCCTTTAGTGATACAGTGTGATTAACCGCGTGTGAATTCGTCCTCATTCGG 458  
DB 311 ACCATGCCCTTTAGTGATACAGTGTGATTAACCGCGTGTGAATTCGTCCTCATTCGG 370  
QY 459 CTCTCCTCACCCCTTACTTCTTGAATATACAGCATCGAAGCACCATGCAACACAA 518  
DB 371 CTCTCCTCACCCCTTACTTCTTGAATATATAGCCATCGAATACCATGCGAACACAA 430  
QY 519 ATTCACTCGAAACGAGGAGTTTACATCTCTAGAACTCAGTCCAGCTCAGGACTTACT 578  
DB 431 ATTCACTCGAACGAGGAGTTTACATCTCTAGAACTCAGTCCAGCTCAGGACTTACT 490  
QY 579 CCACATACGAATTTCTTGAACACACGCCCTGGTTCGAATCTCTATCTTGGTGCATCATGTTAA 638  
DB 491 CCA-----AAATCCTTAACCAACCCACCTGGACGAGTGTCTACTTTGGTTTTCAGGTGA 544  
QY 639 CTTAGGATTTCTTTATACCTCTTAACGAATGTTTTCAGCAAGAGTAGATAGATTTA 698  
DB 545 CGCTAGGGTTTCTTTGATCCTGTTAACTAATATCTCTGAAAGAAATACCAACGGTTTG 604  
QY 699 CCAACCATTTTGATTCATTCAGCCCGATCTTACCGAGCGTGAAGCAATCCAGTTGCGT 758  
DB 605 CCAACCATTTTGATTCATTCAGTCCCATCTTACCAGGCGTGACGAATTCAGTTCCTTG 664  
QY 759 TATCAGATCTTGATCTGTTGCACTGTTTTCAGGACTCAAGTTCCTTGACAAACAAAG 818  
DB 665 TATCAGATCTTGATCTGTTGCACTGTTTTCAGGACTCAAGTTCCTTGACAAACAAAG 724  
QY 819 GATTTGGTGGTGATGTGATGTAGTGTTCAGTGTAGTGTGATGTGATGTGATGTGATGTG 878  
DB 725 GAGCTGTCTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 784  
QY 879 TCGTATCACTTATCTGCAACACACATCTGTCGTCACCCATTACGATTCACCCGAT 938  
DB 785 TTTTGATCAGTATTTTACACACACCCATCTCTCTTACTCTATTCAGATTCAGTTCAGT 844  
QY 939 GGAATCGGATCAAGGAGCGCTTCACCAACATCGACAGATTTTCGGTCTCCTGAATCGGG 998  
DB 845 GGAATCGGATCAAGGAGCGCTTCACCAACATCGATAGGATTTTGGTCTCTTAATAGG 904  
QY 999 TTTTCCAGCGTTTACACACCCAGTGTGTGACCATTTTGTTCCTTCATTCACATTC 1058  
DB 905 TTTTCCAGCGTTTACACACCCAGTGTGTGACCATTTTGTTCCTTCATTCACATTC 964  
QY 1059 ATCATCCAAAGGAGGCAAGCGGCGCATCAAGCCATCTTGGTGTATTCAGGATCATCG 1118  
DB 965 ATCATCCAAAGGAGGCAAGGATGCAATCAACAGTTCCTTGGTGTATTTATTAAGATG 1024  
QY 1119 ACAGGACTCCATTTTTCAAAGCAATGTGGAGAGGCGCAAGGAATGCATTTTACATCGAGC 1178

DB 1025 ATAGGACTCCGATATTTCAAGCAATGTGGAGAGAGCCCAAGGAATGCATCTATCGAGC 1084  
QY 1179 AAGATGCGACAGCAGCAAGCAAAAGGACATATTGGTACCATAAAATGTAA 1228  
DB 1085 CAGATGAAGATACTGAACACAAGGGTGTCTTACTGTGTACCATTAATGTGA 1134  
RESULT 7  
AAF8311  
ID AAF8311 standard; DNA; 1285 BP.  
XX AAF8311;  
DT 22-AUG-2001 (first entry)  
XX C. officinalis calendulic acid desaturase encoding DNA.  
XX Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;  
KW triglyceride; transgenic plant; ds.  
XX Calendula officinalis.  
XX Key Location/Qualifiers  
CDS 42..1175  
/\*tag= a  
/product= "calendulic acid desaturase"  
XX DE19941609-A1.  
XX 08-MAR-2001.  
XX 01-SEP-1999; 99DE-01041609.  
XX 01-SEP-1999; 99DE-01041609.  
XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.  
XX Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;  
WPI: 2001-283028/30.  
P-PSDB; AAB70946.  
XX New nucleic acid sequence encoding Calendula officinalis calendulic acid  
desaturase, useful for e.g. producing transgenic plants having oil with  
an increased unsaturated fatty acid content..  
XX Claim 1b; Page 13-15; 22pp; German.  
XX This invention describes a novel isolated nucleic acid sequence (I)  
encoding a Calendula officinalis calendulic acid desaturase polypeptide.  
The invention also describes (I) a process for producing unsaturated  
fatty acids, comprising introducing at least one copy of (I) or (II) into  
an oil-producing organism, growing the organism, isolating oil from the  
organism and releasing fatty acids from the oil; (2) a process for  
producing triglycerides with an increased unsaturated fatty acid content,  
comprising introducing at least one copy of (I) or (II) into an oil-  
producing organism, growing the organism and isolating oil from the  
organism; (3) a process for producing saturated fatty acids, comprising  
introducing at least one nonfunctional copy of (I) or (II) into an oil-  
producing organism, growing the organism, isolating oil from the organism  
and releasing fatty acids from the oil; (4) a process for producing  
triglycerides with an increased saturated fatty acid content, comprising  
introducing at least one nonfunctional copy of (I) or (II) into an oil-  
producing organism, growing the organism and isolating oil from the  
organism; (5) an enzyme capable of converting a diunsaturated fatty acid  
of to a triunsaturated fatty acid. Transgenic organisms (especially  
plants) containing one or more copies of (I) are useful for producing  
oils with an increased unsaturated fatty acid content. Transgenic  
organisms (especially plants) containing one or more nonfunctional copies  
of (I) are useful for producing oils with an increased saturated fatty  
acid content. (I) and fragments of (I) are also useful for isolating  
genomic sequences by homology screening. This sequence encodes the

|          |   |  |
|----------|---|--|
| CC       | calendulic acid desaturase described in the method of the invention       |  |
| XX       |   |  |
| SQ       | Sequence 1285 BP; 364 A; 294 C; 253 G; 374 T; 0 U; 0 Other;               |  |
|          | Query Match 47.9%; Score 673; DB 4; Length 1285;                          |  |
|          | Best Local Similarity 77.2%; Pred. No. 5.6e-157;                          |  |
|          | Matches 833; Conservative 0; Mismatches 240; Indels 6; Gaps 1;            |  |
| Qy       | 159 CGCAATTCCTGTTAAGTGATCTAAAGAAAGCAATCCCTGCAATGCTTCGCGGATCCG 218         |  |
| Db       | 112 CACCGTTACGCTTAAGCGATCTGAAGAAAGCGATTCTCTACCAATTCGCTTTGAGCGATCG 171     |  |
| Qy       | 219 CCGTCTGTCATCTGCTACGTAAGTTTCAGGATCTCATTTATCACCTTCCTTTTATACACGG 278     |  |
| Db       | 172 TCATCCGGTCACTACTATGTTGTCATGATCTCATTTGTCCTATGCTTCTACTACC 231           |  |
| Qy       | 279 TCGCAACACCTACATTCCTCACCTCCCTCTCTAGTTTACTTAGCATGGCGGTTT 338            |  |
| Db       | 232 TTGCAAACACGTATATCCCTCTTATCTTACACCTCTGGCTTACTAGCATGGCCGTTT 291         |  |
| Qy       | 339 ACTGGTTTGGCAATCTTTGCATCTCTCACTGGTTTATGGGTCCTCGGCCATGAATCGCGCC 398     |  |
| Db       | 292 ACTGGTTTGTCAAGCTAGCATCTCTCACCGGCTCTGGGTCATCGGTCACGAATGTGGTC 351       |  |
| Qy       | 399 ATCATGCCCTTTAGTGAGTACCAGTGGATTGATACGCCGCTTGGATTGCTCTCCATTCCG 458      |  |
| Db       | 352 ACCATGCAATTTAGCGACTACCAGTTGATTGATGACATTTGTTGGATTCTGCTCTCATTCGG 411    |  |
| Qy       | 459 CTCCTCTCACCCCTTACTTTTCTTGGAAATACAGCCATCGAAAGCACCATCGAAACACAA 518      |  |
| Db       | 412 CTCCTCTCACCCCGTATTTCTTCTTGGAAATATAGCCAGGNAATCACACGCCAACACAA 471       |  |
| Qy       | 519 ATTCACTCGAAAGAGGAAAGTTTACATCTCTAGAACTCAGTCCGAGCTCAGGACTTACT 578       |  |
| Db       | 472 ATTCACTCGATAACGATGAAGTTTACATTTCTTAAACGTAAGTCGAAGGCTCAAGATTTATT 531    |  |
| Qy       | 579 CCACATACGAATTTCTTACACACGCTGTGTCGNAATCTCATCTTGGTCTCATGTGTTAA 638       |  |
| Db       | 532 CCA-----AACTCTTTAAACAATCCACCCGGCGAGTGTTCACTTTGGTGTTCGGTTGA 585        |  |
| Qy       | 639 CTTTAGGATTTCTTTATACCTCTTAAGCAATGTTTTCAGGCAAGAGTACGATAGATTTA 698       |  |
| Db       | 586 CTTTAGGATTTCCGTTATACCTCTTAATAATATCTCGGCCAAGAAATACGGAGGTTTG 645        |  |
| Qy       | 699 CCAACCACTTTGATCCATTGAGCCCGATCTTCACCGAGCGTGAGGAAATCCAGGTTGCGT 758      |  |
| Db       | 646 CCAACCACTTTGATCCCATGAGTCCAAATTTTCAACGATCGTGAACGCGTTCAAGTTTTCG 705     |  |
| Qy       | 759 TATCAGATCTTGGTATCGTTGCGAGTGTGTTTACGGACTCAAGTTTCTTGTACAAACAAAG 818     |  |
| Db       | 706 TATCCGATTTCCGTTCTTCTCGCTGTAATTTTATGCAATCAAGCTTCTTGTAGCAGCAAG 765      |  |
| Qy       | 819 GATTTGGTGGTGATGTGCAATGATGGAGTTCCAGTGTATAGGCTCTGAATTCCTTCATTA 878      |  |
| Db       | 766 GGGCAGCTTGGGTATCAACATGACGCAATTCAGTACTAGGTGTAAAGCGTGTCTTCG 825         |  |
| Qy       | 879 TCGTAATCACTTATCTGCACACACACATCTGTCTGTACCCCATTAACGATTCACACCGAAT 938     |  |
| Db       | 826 TTTTGTATCACATATTTGCAACACACCCATCTCTCACTCCCTCATTTATGATTCACACCGAAT 885   |  |
| Qy       | 939 GGAATCGGATCAAGAGGCGTTGACCAATCGACAGAGATTTCCGTTCTCTGTAATCCGG 998        |  |
| Db       | 886 GGAATCGGATCAAGAGGCGCTTATCAACAAATCGATAGGGAATTCGGGTTCTCTGTAATCCGG 945   |  |
| Qy       | 999 TTTTCCAGAGGTTTACACACACCCACCGTGTGTCACCATTTTGTTCCTTACATTCACATTT 1058    |  |
| Db       | 946 TTTTCCAGAGGTTTACACACACTCAGCTCTTGATCTTGATCTCATATTCATTCACATTT 1005      |  |
| Qy       | 1059 ATCATGCAAGAGGCAAGCGAGGCGCATCAAGCCAAATCTTGGTGAATTACAGGATGATCG 1118    |  |
| Db       | 1006 ATCATGCAAGAGGCAAGGATGCAATCAAGCCAGTGTGTCGCGGAGTACTATAAATCG 1065       |  |
| Qy       | 1119 ACAGGACTCCATTTTTCAAAGCAATGTGAGAGAGGCCAAGGAATGCATTTTACATCGAGC 1178    |  |
| Db       |   |  |
| Db       | 1066 ACAGGATCCAAATTTTCAAGCATGTATAGAGAGGCTTAGGATGCATCTACATCGAGC 1125       |  |
| Qy       | 1179 AAGATCGAGACAGCAAGCAAAAGGACATATTGTTGTTACCAATAAATGTAATCGATGATG 1237    |  |
| Db       | 1126 CCGATGAGGATAGCGAGCACAAAGGTGTTCTGTTACCAACAGATGTAATCAAAAAGG 1184       |  |
| RESULT 8 |   |  |
| ADR87352 |   |  |
| ID       | ADR87352 standard; cDNA; 1134 BP.   |  |
| XX       | AC ADR87352;  |  |
| XX       | 18-NOV-2004 (first entry)   |  |
| DT       |   |  |
| XX       | Codon optimised hydroxylase/ epoxygenase coding sequence, SEQ ID 33.      |  |
| DE       |   |  |
| XX       | Nematocide; Plant; 16C monounsaturated fatty acid;                        |  |
| KW       | 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;           |  |
| KW       | fatty acid epoxygenase; fatty hydroxylase; phospholipid:diacylglycerol;   |  |
| KW       | acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;            |  |
| KW       | hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;     |  |
| KW       | nematode; gene; ss.   |  |
| XX       | Stokesia laevis.  |  |
| OS       | Synthetic.  |  |
| XX       |   |  |
| FH       | Key Location/Qualifiers   |  |
| FT       | 1..1134   |  |
| FT       | /*tag= a  |  |
| FT       | /product= "Codon optimised Hydroxylase/ epoxygenase"                      |  |
| XX       |   |  |
| PN       | WO2004071168-A2.  |  |
| XX       |   |  |
| PD       | 26-AUG-2004.  |  |
| XX       |   |  |
| PF       | 04-FEB-2004; 2004WO-US003254.   |  |
| XX       |   |  |
| PR       | 05-FEB-2003; 2003US-0445293P.   |  |
| XX       | (DIVE-) DIVERGENCE INC.   |  |
| XX       | Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;          |  |
| PI       | Hresko MC, McIaird MB, Zentella R;  |  |
| XX       |   |  |
| DR       | WPI; 2004-634973/61.  |  |
| DR       | P-PSDB; ADR87361.   |  |
| XX       |   |  |
| PT       | Novel transgenic plant containing DNA construct having nucleic acid       |  |
| PT       | encoding polypeptide for catalyzing conversion of substrate to            |  |
| PT       | monounsaturated fatty acid product, useful for controlling nematodes.     |  |
| XX       |   |  |
| PS       | Claim 74; SEQ ID NO 33; 180pp; English.                                   |  |
| XX       |   |  |
| CC       | The present invention relates to transgenic plants (I) containing one or  |  |
| CC       | more DNA constructs. The DNA constructs have a nucleic acid encoding a    |  |
| CC       | protein effective for catalyzing the conversion of a substrate to a 16C,  |  |
| CC       | 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid          |  |
| CC       | epoxygenase or a fatty hydroxylase, and a regulatory element operably     |  |
| CC       | linked to the nucleic acid encoding the protein, where the regulatory     |  |
| CC       | element confers expression in vegetative tissue of the plant. The fatty   |  |
| CC       | acid epoxygenase or a fatty hydroxylase can be                            |  |
| CC       | phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol      |  |
| CC       | acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty     |  |
| CC       | acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in |  |
| CC       | a vegetative tissue. The DNA construct of (I) is useful in the production |  |
| CC       | of hydroxylases and epoxygenases that controls nematode damage in         |  |
| CC       | commercially important plant species and so (I) exhibits increased        |  |
| CC       | resistance to nematodes. (I) provides an effective, environmentally safe  |  |
| CC       | methods of inhibiting nematode metabolism, growth, viability,             |  |
| CC       | development, infectivity and/or the nematode life cycle. (I) provides     |  |
| CC       | season-long nematode control, thus providing labor savings, by reducing   |  |

CC the need for and frequency of chemical control. The present sequence is  
CC the coding sequence for one such fatty acid epoxigenase and fatty  
CC hydroxylase, which has been codon optimised for improved plant  
CC expression.  
XX  
SQ Sequence 1134 BP; 299 A; 259 C; 225 G; 351 T; 0 U; 0 Other;  
Query Match 47.3%; Score 665.6; DB 13; Length 1134;  
Best Local Similarity 77.1%; Pred. No. 3.8e-155;  
Matches 825; Conservative 0; Mismatches 239; Indels 6; Gaps 1;  
QY 159 CGCCATTCGTTAGTGAATCAAGAAAGCAATCCCTGCACATTCCTCCGGCGATCCG 218  
DB 71 CACCTTTTCATTAAGTGAATATAAGAAAGCAATCCCTCCCATTCCTCAAAAGGTCTG 130  
QY 219 CGCTCTGGTCACTCTGCTAGTGTTCAGGATCTCAATATACATTCCTCTCTTATACAGG 278  
DB 131 TCATAGGTTCTCATCTACTATGTGTTCATGATCTCATCTCTCTCTCTCTCTCTCTCC 190  
QY 279 TCGCCAAACCTACATTCCTCCACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 338  
DB 191 TCGCAACTACATATATCT 250  
QY 339 ACTGGTTTGGCAATCTTCATCT 398  
DB 251 ACTGGTTTGGCAAGCAAGTATCT 310  
QY 399 ATCATGCTTTAGTGAATCAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 458  
DB 311 ACCATGCTTTAGTGAATCAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 370  
QY 459 CTCTCTCTCACT 518  
DB 371 CTCTCTCACT 430  
QY 519 ATTCACTGAAACGAGGAAGTTTACATCTCTAGAACTCAGTCCCGAGCTCAGCACTTACT 578  
DB 431 ATTCACTGACAAACGAGGAAGTTTACATCTCTAGAACTCAGTCCCGAGCTCAGCACTTACT 490  
QY 579 CCACATACCAATTTCTTGACACACGCTGTTGCAATCTCTCTCTCTCTCTCTCTCTCTCT 638  
DB 491 CCA-----AATCTTAAACACCCACCTGGAAGGGTGTCTCTCTCTCTCTCTCTCTCTCT 544  
QY 639 CTTAGGATTTCTCTTATACCTTTAAACGAATGTTTTCAGGCAAGAGTACGATAGATTTA 698  
DB 545 CTCTAGGGTTTCTCTTGTACCTGTTAACTTAATATCTCTGAAAGAAATACCAAGGTTTG 604  
QY 699 CCAACCATTTGATTCATTCAGCCGATCTTCAACGAGCGTGAGCGAATCCAGGTTGCT 758  
DB 605 CCAACCATTTGATTCATTCAGTCCCATCTTCAACGAGGGAAGGATTCAGGTTCTTG 664  
QY 759 TATCAGATCTTGGTATCGTTGAGTGTGTTTACGACTCAAGTTCTTGTACAAACAAAG 818  
DB 665 TATCAGATCTTGGTCT 724  
QY 819 GATTTGGTGGGTGATGTCATGTATGAGTGTCCAGTGTAGTCTCGAATTCCTTCAATTA 878  
DB 725 GAGTGTCTGGGTGACATGATCTATGAGTGTCCAGTCTCTAGTGTAAAGGTTTCTTCTG 784  
QY 879 TCGTAATCACTTATCTGCAACCAACATCTCTGTGTCACCCCATTAAGTCAACCGAAT 938  
DB 785 TTTTGTATCACTTACTTGTGCAACCAACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 844  
QY 939 GGAATGGATCAAGAGGCTTGACACATCGACAGATTCGCTCTCTCTCTCTCTCTCTCTCT 998  
DB 845 GGAATGGATCAAGAGGCTTGATGCAACCATCGATAGGATTTGGGTTCTCTCTCTCTCTCT 904  
QY 999 TTTTCCACGAGTTTACACACACCCAGTGTGTGACCAATTTGTTCTCTCTCTCTCTCTCT 1058  
DB 905 TTTTCCATGAGTTTACACACATCTATGATGATGATGATGATGATGATGATGATGATGATG 964  
QY 1059 ATCATGCAAGGAGGCAAGCGGCGCATCAAGCCAACTCTTGGGTGATTAACGATGATCG 1118

DB 965 ATCATGCAAGGAGGCAAGCAAGATGCAATCAACCAAGTTTGGTGTATTTATTAAGATTG 1024  
QY 1119 ACAGGACTCCATTTTTCAAAGCAATGTGGAGAGAGCCCAAGGAATGCAATTTACATCGAGC 1178  
DB 1025 ATAGGACTCTTATATTTCAAAGCAATGTGGAGAGAGCCCAAGGAATGCAATCTATATCGAGC 1084  
QY 1179 AAGATGCAAGCAAGCAAGCAAGGACATATTTGGTACCATTAATAATGTAA 1228  
DB 1085 CAGATGAAGATACTGAACACCAAGGGTGTCTTACTGGTACCATTAATAATGTAA 1134  
RESULT 9  
AEC02266  
ID AEC02266 standard; cDNA; 1134 BP.  
XX  
AC AEC02266;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE Stokesia laevis epoxigenase encoding cDNA SEQ ID NO:33.  
XX  
KW transgenic plant; antheimintic; epoxigenase; gene; ss.  
XX  
OS Stokesia laevis.  
XX  
FH Key Location/Qualifiers  
FT 1..1134  
FT /\*tag= a  
FT /product= "epoxigenase"  
XX  
PN US2005172358-A1.  
XX  
PD 04-AUG-2005.  
XX  
PF 04-AUG-2004; 2004US-00912534.  
XX  
PR 04-FEB-2004; 2004US-00772227.  
XX  
PA (VERB/) VERBSKY M L.  
PA (BAUB/) BAUBLITE C.  
PA (KLOE/) KLOE A P.  
PA (DAVI/) DAVILA-APONTE J A.  
PA (HRES/) HRESKO M C.  
PA (MCLA/) MCLAIRD M B.  
PA (ZENT/) ZENTELLA R.  
PA (WILL/) WILLIAMS D J.  
XX  
PI Verbsky ML, Baublite C, Kloeck AP, Davila-Aponte JA, Hresko MC;  
PI Mclaird MB, Zentella R, Williams DJ;  
XX  
DR WPI: 2005-603337/62.  
DR P-PSDB; AEC02275.  
XX  
PT New transgenic plant having a DNA construct comprising a nucleic acid  
PT encoding a protein for catalyzing the conversion of a substrate to a C16,  
PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
PT antheimintic compounds.  
XX  
PS Claim 74; SEQ ID NO 33; 130pp; English.  
XX  
CC The invention relates to a transgenic plant containing at least one DNA  
CC construct comprising: (a) a nucleic acid encoding a polypeptide effective  
CC for catalyzing the conversion of a substrate to a C16, C18, or C20  
CC monounsaturated fatty acid product; and (b) a regulatory element operably  
CC linked to the nucleic acid encoding the polypeptide and conferring  
CC expression in a vegetative tissue of the plant. Also described: (1) a  
CC method of making a transgenic plant; (2) a recombinant nucleic acid  
CC comprising the nucleotide sequence; (3) an isolated nucleic acid  
CC construct comprising at least one regulatory element that confers  
CC expression in a vegetative tissue of a plant; and (4) a method of  
CC screening a transgenic plant for antheimintic activity. The transgenic  
CC plant is useful in preparing compounds having antheimintic activity. The  
CC present sequence encodes an epoxigenase which is used in the

|           |   |   |      |
|-----------|---|---|------|
| CC        | exemplification of the present invention.                                 |   |      |
| XX        | Sequence  | 1134 BP; 299 A; 259 C; 225 G; 351 T; 0 U; 0 Other;            |      |
| XX        | Query Match   | 47.3%; Score 665.6; DB 14; Length 1134;                       |      |
| XX        | Best Local Similarity   | 77.1%; Pred. No. 3.8e-155;                                    |      |
| XX        | Matches   | 825; Conservative 0; Mismatches 239; Indels 6; Gaps 1;        |      |
| Qy        | 159   | CGCATTCCTGTTAAGTGATCTAAAGAAAGCAATCCCTGCAATGCTTCGGCGATCCG      | 218  |
| Db        | 71  | CACCTTTTACATTAAGTGATATAAGAAAGCAATCCCTCCCATTTGCTTCAAAAGGCTG    | 130  |
| Qy        | 219   | CGTCTGTCATCTCTGCTACGTAGTTTACAGATCTCAATATCACCTTCTTTTATACACGG   | 278  |
| Db        | 131   | TCATAAGGTCTTCACTACTATGTTGTCATGATCTCATCGTCTCTACGTCTTCTTCTTCC   | 190  |
| Qy        | 279   | TGCGCAACACCTACATTCCTCACCTCCCTCTCTCTAGTTTACTTAGCATGGCGGTTT     | 338  |
| Db        | 191   | TGCGCACTACATATATTAATGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT    | 250  |
| Qy        | 339   | ACTGGTTTTGGCAATCTTTGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT    | 398  |
| Db        | 251   | ACTGGTTTTGGCAAGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 310  |
| Qy        | 399   | ATCATGCTTTAGTGAGTACAGTGGATTTGATTAAGCGCGTTGGATTCGTCTCTCTCTCG   | 458  |
| Db        | 311   | ACCATGCTTTAGTGAATACCAAGTGGATTTGATGACACAGTTGGGTTCTCTCTCTCTCT   | 370  |
| Qy        | 459   | CTCTCTCACCCCTTACTTTTCTTGGAAATACAGCATCGAAAGCACCACATCAACACAA    | 518  |
| Db        | 371   | CTCTCTCACCCCTTACTTTCTTGGAAATATAGCCATAGGAATCACCATGCTAACACAA    | 430  |
| Qy        | 519   | ATTCATCGAAACAGGAAAGTTTACATTCCTCTAGAACTCAGTCCCGAGCTCAGGACTTACT | 578  |
| Db        | 431   | ATTCATCGAACAGCAAGTTTACATTCCTTAAGAGGAAGTCCAAAGTCAAGACTTACT     | 490  |
| Qy        | 579   | CCACATAGCAATTTCTTGACAAACAGCGCTGTGCAATCTCTATCTTGTGTCATCATTTAA  | 638  |
| Db        | 491   | CCA-----AAATCTAAACAAACCCACCTGGAAGGGTGTTCACTTTGGTTTTTCAAGTTGA  | 544  |
| Qy        | 639   | CCTTAGGATTTCTTTATACCTTTTAAAGAAATGTTTTCAGGCAAGAGTACGATAGATTTA  | 698  |
| Db        | 545   | CTCTAGGGTTTCTTTTACCTGTTTAACTATCTCTGGAAGAAATACCAAGGTTTG        | 604  |
| Qy        | 699   | CCAACCACTTTGATCATTGAGCCCGATCTTTCACCGAGCGTTCAGCGAATCCAGGTTGGT  | 758  |
| Db        | 605   | CCAACCACTTTGATCATTGAGTCCCATCTTTCACCGAGGAGGAAGGATTCAGGTTCTTG   | 664  |
| Qy        | 759   | TATCAGATCTTGGTATCGTTGTCAGTGTGTTTACGAGTCAAGTTTCTTGTACAAACAAAG  | 818  |
| Db        | 665   | TATCAGATCTTGGTCTTCTAGCTGTAAATCTAGGCAATCAAGCTTCTTGTGTCGCAAG    | 724  |
| Qy        | 819   | GATTTGGTTGGTGATGTCATGTATGAGTTTCCAGTGTATAGTCTGAAATTCCTTCATTA   | 878  |
| Db        | 725   | GAGCTGTCTGGTGATCATGTCATGATGAGTTTCCAGTCTTAGTGTAAGCGTGTCTTCG    | 784  |
| Qy        | 879   | TGTTAATCACTTATCTGCACCAACACATCTGTCTCACCCCATTCAGATTCACACCGAAT   | 938  |
| Db        | 785   | TTTTGATCACTTACTTTCACCAACACCCATCTTCTCTGCTCATTCAGATTCCTAGT      | 844  |
| Qy        | 939   | GGAATCGATCAAGAGCGCTTGACCAATTCGACAGAGATTTTGGTCTCTCTGATTCGGG    | 998  |
| Db        | 845   | GGAATCGATCAGAGGGGCTTGTCAACCATCGATAGGGAATTTGGGTTCTCTTAATAGGG   | 904  |
| Qy        | 999   | TTTTTCCAGGTTTACACACACCCAGTGTGTCACCATTTGTTCTCTTACATTCACATTT    | 1058 |
| Db        | 905   | TTTTTCCAGGTTTACACACTCATGATGATGATGATGATGATGATGATGATGATGATGAT   | 964  |
| Qy        | 1059  | ATCATGCAAGAGGAGCAAGCGGCGCATCAAGCCCAATCTTGGGTGATTTACAGGATGATCG | 1118 |
| Db        | 965   | ATCATGCAAGAGGAGCAAGAGATGCAATCAACACCAAGTTTGGGTGATTTATTAAGATTG  | 1024 |
| Qy        | 1119  | ACAGGACTCCATTTTTCAAAGCAATGTGAGAGAGGCGCAAGGAATTCATTTACATCGAGC  | 1178 |
| Db        | 1024  | ACAGGACTCCATTTTTCAAAGCAATGTGAGAGAGGCGCAAGGAATTCATTTACATCGAGC  | 1178 |
| Db        | 1084  | ATAGGACTCTCTATATTCAAGCAATGTGAGAGAGGCGCAAGGAATTCATTTACATCGAGC  | 1084 |
| Qy        | 1179  | AAGATGCAGACAGCAAGCAACAAAGGGACATATTGGTACCAATAAATGTAA           | 1238 |
| Db        | 1085  | CAGATGAAGATACTGAACACAAAGGGTGTCTTACTGTTACCAATAAATGTAA          | 1134 |
| Db        | 1085  | CAGATGAAGATACTGAACACAAAGGGTGTCTTACTGTTACCAATAAATGTAA          | 1134 |
| RESULT 10 |   |   |      |
| ADR87325  |   |   |      |
| ID        | ADR87325  | standard; cDNA; 1125 BP.                                      |      |
| XX        | ADR87325;   |   |      |
| AC        | ADR87325;   |   |      |
| DT        | 18-NOV-2004   | (first entry)   |      |
| XX        | Hydroxylase/ epoxigenase coding sequence, SEQ ID 6.                       |   |      |
| DE        | Nematocide; Plant; 16C monounsaturated fatty acid;                        |   |      |
| XX        | 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;           |   |      |
| KW        | fatty acid epoxigenase; fatty hydroxylase; phospholipid:diacylglycerol;   |   |      |
| KW        | acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;            |   |      |
| KW        | hydroxy-fatty acid; ricinoleic acid; epoxyl-fatty acid; vernolic acid;    |   |      |
| KW        | nematode; gene; ss.   |   |      |
| XX        | Crepis biennis.   |   |      |
| OS        | Crepis biennis.   |   |      |
| XX        | Key   | Location/Qualifiers   |      |
| FT        | CDS   | 1..1125   |      |
| FT        |   | /*tag= a  |      |
| FT        |   | /product= "Hydroxylase/ epoxigenase"                          |      |
| XX        | WO2004071168-A2.  |   |      |
| XX        | 26-AUG-2004.  |   |      |
| XX        | 04-FEB-2004; 2004WO-US003254.   |   |      |
| XX        | 05-FEB-2003; 2003US-0445293P.   |   |      |
| XX        | (DIVE-) DIVERGENCE INC.   |   |      |
| XX        | Verbsky ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;          |   |      |
| XX        | Hresko MC, McIaird MB, Zentella R;  |   |      |
| XX        | WPI; 2004-634973/61.  |   |      |
| XX        | P-PSDB; ADR87337.   |   |      |
| XX        | Novel transgenic plant containing DNA construct having nucleic acid       |   |      |
| XX        | encoding polypeptide for catalyzing conversion of substrate to            |   |      |
| XX        | monounsaturated fatty acid product, useful for controlling nematodes.     |   |      |
| XX        | Claim 74; SEQ ID NO 6; 180pp; English.                                    |   |      |
| XX        | The present invention relates to transgenic plants (I) containing one or  |   |      |
| XX        | more DNA constructs. The DNA constructs have a nucleic acid encoding a    |   |      |
| XX        | protein effective for catalyzing the conversion of a substrate to a 16C,  |   |      |
| XX        | 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid          |   |      |
| XX        | epoxigenase or a fatty hydroxylase, and a regulatory element operably     |   |      |
| XX        | linked to the nucleic acid encoding the protein, where the regulatory     |   |      |
| XX        | element confers expression in vegetative tissue of the plant. The fatty   |   |      |
| XX        | acid epoxigenase or a fatty hydroxylase can be                            |   |      |
| XX        | phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol      |   |      |
| XX        | acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty     |   |      |
| XX        | acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in |   |      |
| XX        | a vegetative tissue. The DNA construct of (I) is useful in the production |   |      |
| XX        | of hydroxylases and epoxigenases that controls nematode damage in         |   |      |
| XX        | commercially important plant species and so (I) exhibits increased        |   |      |
| XX        | resistance to nematodes. (I) provides an effective, environmentally safe  |   |      |
| XX        | method of inhibiting nematode metabolism, growth, viability,              |   |      |
| XX        | development, infectivity and/or the nematode life cycle. (I) provides     |   |      |
| XX        | season-long nematode control, thus providing labor savings, by reducing   |   |      |
| XX        | the need for and frequency of chemical control. The present sequence is   |   |      |



CC plant is useful in preparing compounds having anthelmintic activity. The  
CC present sequence encodes an epoxigenase which is used in the  
CC exemplification of the present invention.

XX  
SQ Sequence 1125 BP; 285 A; 277 C; 234 G; 329 T; 0 U; 0 Other;

Query Match 46.8%; Score 657.8; DB 14; Length 1125;  
Best Local Similarity 75.6%; Pred.No. 3.3e-153;  
Matches 847; Conservative 0; Mismatches 262; Indels 12; Gaps 2;

QY 108 ATGATCGAATGAAGATCATGATATGAGCAAGAGCCCGGATGATCGCGCGCATCTCT 167  
DB 17 ATGGTCGAACATCGAAGAAATCGGTGATGGAACGGTCTCGTTGATCCAGTACCCITCT 76  
QY 168 CGTTAAGTGATCTAAGAAAGAAATCCCTGACATATGCTTCGGCGATCCCGCTCTGGT 227  
DB 77 CGCTAAGTGATTTAAGCAAGCAATCCCTCCCGATGCTTCGAGCGATCTGTCATCCGTT 136  
QY 228 CATCTGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 287  
DB 137 CATCTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196  
QY 288 CCTACATTCCTCACCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 347  
DB 197 AATATATTCGGATTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 256  
QY 348 GCCAATCTTGATCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 407  
DB 257 GTCAGCTAGCATCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 316  
QY 408 TTAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 467  
DB 317 TTAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 376  
QY 468 CCCCTTACTTTCTTGGAAATACAGCATCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 527  
DB 377 CCCGATTTCTGTTGAAATACAGTACCGGATCACCATGCGCAAGCAAGCAAGCAAGCA 436  
QY 528 AAAAGGAGAAAGTTTACATCTCTAGAACTCAGTCCAGCTCAGGACTTACTCCACATACG 587  
DB 437 ATAAGCATGAAAGTTTACATCTCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 490  
QY 588 AATTTCTTGACAAACAGCTGTCGAATCCTCATCTTGGTATCATGATGATTAACCTTAGAT 647  
DB 491 AACTTCTTAAACACCGCTGTCGACTGTTAGTTATGTTATGTTATGTTATGTTATGTTAT 550  
QY 648 TTCTTTTATACCTTTAAGCAATGTTTCAGGCAAGATGATGATGATGATGATGATGATG 707  
DB 551 TTCTTTTATACCTTTGACAAATATTTTCGGCAAGATGATGATGATGATGATGATGATG 610  
QY 708 TTGATCCATTTAGCCCGATCTTACCGAGCGTGAAGCAATCCAGGTTGCGTTTATCAGATC 767  
DB 611 TCGACCCCATGATGATCAATTTTCAAGGAAGCTGAGCGGTTTCAGGTTCTGCTTTCCGATC 670  
QY 768 TTGGTATGTTGCACTGTTTACGAGCTCAAGTTCTTGTACAAACAAAGATTTGGTT 827  
DB 671 TTGGCTTTCTGCTGTTTATGGAATTTAAAGTTTGTGTAGCAAGAAAGAGAGTGGGT 730  
QY 828 GGGTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 887  
DB 731 GGGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790  
QY 888 CTTATCTGACACACATCTGCTGCTCACCCTTATGATTTCAACCGAATGGAATCGGA 947  
DB 791 CGTACTTGACACACACCATCATGCTGCTCCTCATTTATGATCACTCAACTGAATGGA 850  
QY 948 TCAAGAGAGCTTGACCAACATCGACAGATTTTGGGTTCTCTGATCGGTTTTCACG 1007  
DB 851 TCAGAGGGGCGTTGTGACCAATTCGATAGGACTTTTGGGTTTCATGAATAGTGTTC 910  
QY 1008 AGTTTACACACACACCGCTGTTGACCAATTTGTTTCCCTACATTCACATTCATCATG 1067  
DB 911 ATGTTACACACACTCAGCTGATGATCATATGTTTTCATACATTCACACTATCATGGA 970

QY 1068 AGAGGCAAGCGAGGCCCATCAAGCCATCTTGGTGATTACAGGATGATCGACAGGACTC 1127  
DB 971 AAGAGGCAAGGGATGCAATCAATCAATCATAGCGGACTATTATGATCGATAGGACTC 1030  
QY 1128 CATTTTCAAAGCAATGTGAGAGAGGCCCAAGGAATGCATTTATCATCGACGAAGATGCG 1187  
DB 1031 CAATTTTGAAGCACTGTGAGAGAGGCCCAAGGAATGCATGTATCATCGAGC-----CTG 1084  
QY 1188 ACAGCAAGCAAAAGGACATATTGGTACCATAAAATGTAA 1228  
DB 1085 ATAGCAAGCGCAAGGTGTATATTGGTACCATAAAATGTGA 1125

RESULT 12  
AAV63102

ID AAV63102 standard; cDNA; 1312 BP.

XX AAV63102;

AC AAV63102;

DT 02-FEB-1999 (first entry)

XX Crepis sp. delta-12-epoxigenase cDNA clone Crepx.

DE Fatty acid epoxigenase; Crepx; delta-12-epoxigenase;

XX mixed function monooxygenase; epoxysenated fatty acid; transgenic plant;

KW vegetable oil; oilseed; ss.

XX Crepis sp.

PH Key Location/Qualifiers

FT CDS 26..1150

FT /\*tag= a

XX WO9846762-A1.

PD 22-OCT-1998.

XX 09-APR-1998; 98WO-AU000246.

XX 15-APR-1997; 97AU-00006223.

PR 15-APR-1997; 97AU-00006226.

PR 16-APR-1997; 97US-0043706P.

PR 20-JUN-1997; 97US-0050403P.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (STYM/) STYMNE S.

PI Stymne S, Green A, Singh S, Lenman M;

XX WPI; 1998-568734/48.

DR P-PSDB; AAW79743.

XX New isolated fatty acid epoxigenase gene - used particularly for

PT transforming plants for producing modified oils for use in, e.g.

PT coatings, resins, glues, plastics, surfactants or lubricants.

XX Claim 16; Page 84-86; 150pp; English.

XX This cDNA clone, designated Crepx, codes for a novel epoxigenase (see

CC AAW79743) of a Crepis sp. (not Crepis palaestina) that has a high

CC vernolic acid content. The Crepx gene shows a high degree of homology to

CC the novel Cpald delta-12-epoxigenase gene (see AAV63101) of C.

CC palaestina. Crepx cDNA was isolated from a Crepis sp. cDNA library using

CC a Crepis alpina acetylenase partial gene sequence (see AAV63104) as

CC probe. The invention relates generally to novel genetic sequences (see

CC AAV63101-03) encoding fatty acid epoxigenases (see AAW79742-44),

CC especially delta-12-epoxigenases or mixed function monooxygenases. These

CC provide the means by which fatty acid metabolism can be manipulated in

CC e.g. yeast, mould, bacteria, insects, birds, mammals and plants

CC (especially oilseed plants such as flax), in particular to convert

CC unsaturated fatty acids to epoxysenated fatty acids. The invention

CC extends to genetically modified oil-accumulating organisms and to the

CC oils derived from them. These oils can be used in production of coatings,  
resins, glues, plastics, surfactants or lubricants

XX  
SQ Sequence 1312 BP; 347 A; 301 C; 263 G; 399 T; 0 U; 2 Other;

Query Match 46.8%; Score 657.6; DB 2; Length 1312;  
Best Local Similarity 76.4%; Pred. No. 3.8e-153;  
Matches 836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

```
QY 137 GAACGAGCCCGATTCGATCCGGCGCATCTCGTTAAGTGATCTAAAGAAAGCAATCCCT 196
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 GAACGGTCTCAGTTGATCCAGTAACCTTCTCCTGAGTGATTTGAAGCAAGCAATCCCT 130
QY 197 GCACATTTGCTTCGGCGCATCCGCGCTCTGGTTCATCTGCTAGCTAGTTTCAGGATCTCAT 256
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131 CCACATTTGCTTCAGCGCATCTGTTCATCCGTTTCATCTTATTAGTTGTTCCAGGATCTCAT 190
QY 257 ATCACCTTCTTTTATACAGGTGCGCAACACCTACATCTCTCACCTCCCTCTCTCTCTA 316
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191 ATTGCTACATCTTCTACTTCTCTTCCCTTGCCACACATATATCCCTAATCTCCCTCATCTCTA 250
QY 317 GTTTACTTAGCATGGCGGTTTACTGTTTTCGCAATCTTGGCATCTCTCACTGGTTTATGG 376
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 GCTACTTAGCTTGGCGGTTTACTGGTCTGTCAAGCTAGGCTCTCTCACTGGTTATGG 310
QY 377 GTCTCGGCGCATGAATCGCGCCATCATGCTTTTAGTGAGTACAGTGGATTGATACGCC 436
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
311 ATCTCGGCGCATGAATGTGTCCACCATGCTATAGCAACTACACATGGGTTCAGCACACT 370
QY 437 GTTGAATTCGCTTCATTCGGCTCTCTCAACCCCTTACTTTTCTTGGAAATACAGCCAT 496
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
371 GTGGGCTTCATCATCTCATTTCAATTTCTCTCACCCCGTATTCTCTTGGAAATACAGTCAC 430
QY 497 CGAAGCCCATGCAACAACTTCACTCGAAACGAGGAGTTTACATTTCTTAGAACT 556
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGGAATCACCATTCACCAACAAAGTTCGATGATACGATGAAGTTTACATTCGAAAGC 490
QY 557 CAGTCCAGCTCAGGATTTACTCCACATACGAAATTTCTTGAAACACGCGCTGTTCGAATC 616
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
491 AAGTCCAACTCAAGGT-----ATCTATAACTTCTTAACCAACCCACTGTGCACTG 544
QY 617 CTCATCTTGGTCATCATGTTAACTTTAGGATTTCTTTTATACCTTTTAAAGATTTTCA 676
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
545 TTGGTTTGGTTATCATGTTTCACTTAGGATTTCTTTTATACCTTTGACAAATATTTCC 604
QY 677 GGCAGAAGTACGATAGATTACCAACCACTTTGATCCATTGAGCCGATCTTCAACGAG 736
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
605 GGCAGAAGATACGATAGTTTGCACCACTTTCGACCCCATGAGTCCAATTTTCAAGAA 664
QY 737 CGTGAGCGAATCCAGGTTCGGTTTATCAGATCTTGGTATCGTTGAGTGTTTTACGGACTC 796
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
665 CGTGAGCGGTTTCAGTCTTCTTTCGGATCTTGGTCTTCTGCTGTGTTTATGAAAT 724
QY 797 AAGTTTCTTGTACAAACAAAGGATTTGGTGGGTGATGTCATGATGAGGATTCAGTG 856
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
725 AAAGTTGCTGTAGCAATAAAGAGCTGCTTGGGTGGCGTGATGATGAGGATTCGGTG 784
QY 857 ATAGGTCTGAATTCCTTCAATTATCGTAATCACTTATCTGCACACACATCTGTCTCA 916
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
785 CTAGGCGTATTTACCTTTTTCGATGTGATCACTGTTTACACCAACCCATGATGCTG 844
QY 917 CCCATTACGATTTCAACCGAATCGAATCGAATCGAATCGAATCGAATCGAATCGAATCGA 976
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
845 CCTCATATGATTTCAACTGATGGAATCGATGATGAGGGGCTTTGTCAGCAATCGATAGN 904
QY 977 GATTTCCGCTCTCTGAAATCGGTTTTTCCAGAGCTTTACACACACCCAGTGTTCACCAT 1036
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
905 GACTTTGGGTTCTGATAGTGTGTTTCCATGATGTNACACACACTCAGGTTCATGATCAT 964
QY 1037 TTGTTTCCCTCATTTCCATTTATCATGCAAGAGGCAAGCGAGGCCATCAAGCCAAATC 1096
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
965 TTGTTTTCATACATTCACACTATCATGCAAGAGGCAAGGATGCAATCAACACCGATC 1024
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QY 1097 TTGGTGATTCAGGATGATCGACAGGACTCATTTTCAAGCAATGTGGAGAGAGGCC 1156
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1025 TTGGGCGGCTTTTATATGATCGATAGGACTCCCAATTTTAAAGCAATGTGGAGAGAGGCC 1084
QY 1157 AAGGAATCATTTTACATCGAGCAAGATCGACAGCAAGCAAGCAAGGACATATTGGTAC 1216
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1085 AGGAATCATGATCATCGAGC-----CTGATAGCAAGCTCAAGGTGTTTATTGGTAT 1138
QY 1217 CATAAATGTATC 1230
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1139 CATAAATGTATC 1152

RESULT 13
ADR87331
ID ADR87331 standard; cDNA; 1143 BP.
XX
AC ADR87331;
XX
DT 18-NOV-2004 (first entry)
XX
DE PAD2/Hydroxylase/ epoxxygenase coding sequence, SEQ ID 12.
XX
KW Nematocide; Plant; 16C monounsaturated fatty acid;
KW 18C monounsaturated fatty acid; 20C monounsaturated fatty acid;
KW fatty acid epoxxygenase; fatty hydroxylase; phospholipid:diacylglycerol;
KW acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;
KW hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
KW nematode; gene; ss; PAD2.
XX
OS Crepis biennis.
OS Arabidopsis thaliana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1143
FT /tag= a
FT /product= "PAD2/Hydroxylase/ epoxxygenase"
XX
PN WO2004071168-A2.
XX
PD 26-AUG-2004.
XX
PF 04-FEB-2004; 2004WO-US003254.
XX
PR 05-FEB-2003; 2003US-045293P.
XX
PA (DIVE-) DIVERGENCE INC.
XX
PI Verbeke ML, Baublite C, Williams DJ, Kloek AP, Davila-Aponte JA;
PI Hresko MC, Mcclaird MB, Zentella R;
XX
DR WPI; 2004-634973/61.
DR P-PSDB; ADR87343.
XX
PT Novel transgenic plant containing DNA construct having nucleic acid
PT encoding polypeptide for catalyzing conversion of substrate to
PT monounsaturated fatty acid product, useful for controlling nematodes.
XX
PS Claim 74; SEQ ID NO 12; 180pp; English.
XX
CC The present invention relates to transgenic plants (I) containing one or
CC more DNA constructs. The DNA constructs have a nucleic acid encoding a
CC protein effective for catalyzing the conversion of a substrate to a 16C,
CC 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid
CC epoxxygenase or a fatty hydroxylase, and a regulatory element operably
CC linked to the nucleic acid encoding the protein, where the regulatory
CC element confers expression in vegetative tissue of the plant. The fatty
CC acid epoxxygenase or a fatty hydroxylase can be
CC phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol
CC acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty
CC acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in
CC a vegetative tissue. The DNA construct of (I) is useful in the production
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of hydroxylases and epoxigenases that controls nematode damage in commercially important plant species and so (1) exhibits increased resistance to nematodes. (1) provides an effective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, development, infectivity and/or the nematode life cycle. (1) provides season-long nematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is the coding sequence for one such fatty acid epoxigenase and fatty acid hydroxylase used to illustrate the invention. The encoded protein is a fusion protein where the N-terminal sequence of the epoxigenase and hydroxylase has been replaced with the N-terminal sequence of Arabidopsis thaliana FAD2.

Sequence 1143 BP; 291 A; 279 C; 243 G; 330 T; 0 U; 0 Other;

Query Match 45.9%; Score 646; DB 13; Length 1143;

Best Local Similarity 73.8%; Pred. No. 2.8e-150;

Matches 852; Conservative 0; Mismatches 290; Indels 12; Gaps 2;

75 TGGGAGAGGTAGCAGATGTCGGAATTCATATGATGATCGAATGAAGATCATGATATGG 134  
 2 TGGGTGCGAGGTGGAAGATGCGGGTCTCTCTTCCAGAAATCGGAACCGACACCA 61  
 135 ACGAAGAGCCCGGATTCATCGCGCCATCTCGTTAAGTGATCTAAAGAAAGCAATCC 194  
 62 CAAGCGGTGCGGTGCGAAGAACCGCTTTCTCGGTGGAGATCTGAAGAAAGCAATCC 121  
 195 CTGCACATTTGCTTCGGGGATCCGCGCTCTGGTCACTCTGCTAGCTTCAAGGATCTCA 254  
 122 CTCGCCATTTGCTTCAGCGATCTGTAATCGGTTCTACTTATGATGATTCACGATCTCA 181  
 255 TTATCACCTTCTTTTATACAGCGTGGCGAACAACCTATCTCTCCTCCTCCTCTCTC 314  
 182 TTATTTGCTTACATCTTCTACTTCTTGGCGATAATATATCCGATTTCTCCTGCTCTC 241  
 315 TAGTTTACTTAGCATGGCGGTTTACTGTTTGGCAATCTTGCAATCTCTCACTGTTTAT 374  
 242 TAGCTTACTTAGCTTGGGCCCTTTACTGTTCTGTCAGTAGCATCTCTCACTGTTTAT 301  
 375 GGGTCTCGGCGATGAATGCGGCCATCATGCTTTAGTGAGTACGAGTGGATTGATAACG 434  
 302 GGATCTCTCGGTATGAATGCGGTACCATGCTTTAGCGAGCACCAATGGGTTGAGACA 361  
 435 CGTTGGATTTGCTCTCATTTGCGTCTCTCACCCTTATCTTTCTTTGGAAATACAGCC 494  
 362 CTGTGGGCTTCAATGTTCCACTCATTTCTCTCCTCACCCTGATTTCTCTGTTGAATAC 421  
 495 ATCGAAGCAGCATCCAAACACAAATTCATCGAAACGAGGAAGTTTACATCTCTAGAA 554  
 422 ACCGGAATCACCATGCCAACACAAAGTTCATGTATGAAGTGAAGTTTACATCTCGAAA 481  
 555 CTCAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAAACAGCTGGTGGAA 614  
 482 GCAAGTCCAACTCGCGCTT-----ACCTATAAATCTTTAAACACCGCGCTGCTGAC 535  
 615 TCCTCATCTTGTCATCATGTTAACTTAGGATTTCTTTTATACCTCTTAACGAATGTTT 674  
 536 TGTAGTTATGTTATCATGTTTCACTAGGATTTCTTTTATACCTCTTTGACAAATATTT 595  
 675 CAGGCAAGAGTACCATAGATTTTACCAACCTTTGATCCATTTGAGCCGATCTTCAAGG 734  
 596 CCGCAAGAGTACGACAGGTTTGGCAACCATCTCGACCCCATGAGTCCATTTTCAAGG 655  
 735 AGCGTGAGCGAATCCAGGTGCGTTTATCAGATCTTTGGTATCGTTGAGGTTTTCAGGAC 794  
 656 RACGTGAGCGGTTTCAGGTTTGGCTTTCGGATCTTTGGCCCTTCTTCTGTTGTTTATGAA 715  
 795 TCAAGTTTCTTGACAAACAAAGAAATTTGGTGGTGGTATGTCATGATGAGTTCCAG 854  
 716 TTAAGATTGCTGTACAAAGAAAGAGCTGCGTGGGTGGTGTATGATGAGTTCCGA 775  
 855 TGATAGGTTGAATTCCTTCAATTCATGTAATCACTTATCTGCACACACACATCTGTCGT 914

776 TGCTAGCGGTATTTACCTTTTCGATATCATCAGTACTTGACACACACCCATCAGTCGT 835  
 915 CACCCCATTTAGATTTAAACGAATGGAATCGGATCAAAGAGCCTTGACCAATTCGACA 974  
 836 CTCCTCATTTATGACTCAACTGAATGGAATCGGATCAGAGGGGCGTTGTTCAGCAATCGATA 895  
 975 GAGATTTCCGGTCTCTGAAATCGGGTTCCTCAGCAGCTTTACACACACCCAGCTGTTGCACC 1034  
 896 GGGACTTTGGGTTTCAATGAATAGTGTTCATGATGTTTACACACATCTCAGCTCATGATC 955  
 1035 ATTTGTTTCCCTACATTTCCACATTTATCATGCAAGAGGCAAGCGCCATCAAGCCAA 1094  
 956 ATATGTTTTCATATCATTTCCACACTATCATGCAAGAGGCAAGGATGCAATCAATCAACA 1015  
 1095 TCTTGGGTGATTACAGGATGATCAGAGGACTCCATTTTCAAAGCAATGTGGAGAGG 1154  
 1016 TCATAGCGCATATATATGATGATGATAGGACTCCAAATTTTGAAGAGCACTGTGGAGAGG 1075  
 1155 CCAAGGAATGATTTACATCGAGCAAGATGACAGACGACCAAGAGGACATATTGGT 1214  
 1076 CCAAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129  
 1215 ACCATAAAATGTAA 1228  
 1130 ATCATAAATGTGA 1143

RESULT 14  
 AEC02245  
 ID AEC02245 standard; cDNA; 1143 BP.  
 XX  
 AC AEC02245;  
 XX  
 DT 06-OCT-2005 (first entry)  
 XX  
 DE Crepis biennis epoxigenase encoding cDNA SEQ ID NO:12.  
 XX  
 KW transgenic plant; anthelmintic; epoxigenase; gene; ss.  
 XX  
 OS Crepis biennis.  
 XX  
 PH Key Location/Qualifiers  
 CDS 1..1143  
 FT /\*tag= a /product= "epoxigenase"  
 FT  
 XX US2005172358-A1.  
 PN  
 PD 04-AUG-2005.  
 XX  
 PF 04-AUG-2004; 2004US-00912534.  
 XX  
 PR 04-FEB-2004; 2004US-00772227.  
 XX  
 PA (VERB/) VERBSKY M L.  
 PA (BAUB/) BAUBLITE C.  
 PA (KLOE/) KLOEK A P.  
 PA (DAVI/) DAVILA-APONTE J A.  
 PA (HRES/) HRESKO M C.  
 PA (MCLA/) MCLAIRD M B.  
 PA (ZENT/) ZENTELLA R.  
 PA (WILL/) WILLIAMS D J.  
 XX  
 Verbsky ML, Baublite C, Kloek AP, Davila-Aponte JA, Hresko MC;  
 Mclaird MB, Zentella R, Williams DJ;  
 XX  
 WPI; 2005-603337/62.  
 DR P-PSDB; AEC02257.  
 XX  
 PT New transgenic plant having a DNA construct comprising a nucleic acid  
 PT encoding a protein for catalyzing the conversion of a substrate to a C16,  
 PT C18 or C20 monounsaturated fatty acid product, useful in preparing  
 PT anthelmintic compounds.



|    |   |  |
|----|---|--|
| XX | Claim 53; SEQ ID NO 12; 130pp; English.   |  |
| XX | The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The present sequence encodes an epoxigenase which is used in the exemplification of the present invention. |  |
| XX | Sequence 1143 BP; 291 A; 279 C; 243 G; 330 T; 0 U; 0 Other;   |  |
| QY | Query Match   | 45.9%; Score 646; DB 14; Length 1143;                                |
| XX | Best Local Similarity   | 73.8%; Pred. No. 2.8e-150;   |
| XX | Matches   | 852; Conservative 0; Mismatches 290; Indels 12; Gaps 2               |
| QY | 75  | TGGGAGAGGTAGCAGRATGTCGGATTCATATGATGTCGATGAAGATCATGATATCGG 134        |
| DB | 2   | TGGGTGCAGGTGGGAAGATGCCGTTCTCTCTTCCTCCAAAGAAATCGGAAACCGACACCA 61      |
| QY | 135   | ACGAAACAGCCCGCATTTGATCCGGCGCCATTCCTCGTTAAGTGATCTAAAGAAAGCAATCC 194   |
| DB | 62  | CAAAAGCGTGTCCGTGCGNGAAACCGCCCTTCTCGTGGGAGATCTGAAGAAGCAATCC 121       |
| QY | 195   | CTGCACATTTGCTTCGGCGATCCCGCGTCTGGTCACTCTGCTACGTAGTTCAGGAATCTCA 254    |
| DB | 122   | CTCCCCATTTGCTTCAGCGATCTGTAAATCCGTTTCATCTTATGTAGTTCCAGATCTCA 181      |
| QY | 255   | TTATACCTTCTTTTATACAGGTCGCGACACACCTACATCTCTCACCTCCCTCCCTCCCTC 314     |
| DB | 182   | TTATTTGCTTACATCTTCTACTTCTCTGCGGATAAATATATTTCCGATTCCTCCCTGCTCCTC 241  |
| QY | 315   | TAGTTTACTTTAGCATGGCCGGTTTACTCGTTTGTGCAATCTTGCACTCTCACTGGTTTAT 374    |
| DB | 242   | TAGCTTACTTAGCTTTGGCCCTTTTACTGGTTCTGTCAAGTAGCATCTCACTGGTTTAT 301      |
| QY | 375   | GGGTCTCTCGGCATGAATGCGGCCCATCATGCTTTTGTAGTGAGTACCAGTGGATTGATAAGC 434  |
| DB | 302   | GGATCCTCGGTGATGAATGCGGTCAACATGCTTTTGTAGCGAGCACCACCAATGGGTTCAGACA 361 |
| QY | 435   | CCGTTGGAATTCGTCTCATTCGCGTCTCTCACCCCTTACTTTTCTTGGAATAATACAGCC 494     |
| DB | 362   | CTGTGGGGTTCATGGTCCACATCATTTCTCTCCACCCCGTATTTCTCTGTGGAATAACAGTC 421   |
| QY | 495   | ATCGAAGACCATGCGAAACAAATTCACCTCGAAAAACGAGGAGTTTACATCTCTCTAGAA 554     |
| DB | 422   | ACCGGAATCACATGCCAACACAAGTTCCATGTATPACGATGAAGTTTACATCTCGAATA 481      |
| QY | 555   | CTCAGTCCCAGCTCAGGACTTTACTCCACATACGAAATTTCTTGACAAACACGCGCTGGTCGAA 614 |
| DB | 482   | GCAAGTCCAACTCGCGTT-----ACCTATAACTTCTTAAACAACCGCTGGTCGAC 535          |
| QY | 615   | TCCTCATCTCGGTCAATCATGTTAACTTTAGGATTTCTTTTATACCTCTTTAAACGAATGTTT 674  |
| DB | 536   | TGTTAGTTATGTTTATCATGTTTACCTTACAGGATTTCCCTTTATACCTCTTTGACAAATATTT 595 |
| QY | 675   | CAGCAAGAAGTACGATAGATTTACCAACCACTTTGATCCATTGAGCCCGATCTTCACCG 734      |
| DB | 596   | CCGCGCAAGAAGTACGACAGGTTTGGCAACCACTTCGACCCCAATGAGTCCAAATTTTCAAGG 655  |
| QY | 735   | AGCGTGAGCGAATCCAGGTTGCGTTTATCAGATCTTTGGTATCGTTGCGAGTGGTTTTACGGAC 794 |
| DB | 656   | AACGTGAGCGGTTTCAGGCTCTTGCTTCGGATCTTTGGCCCTCTTCTGCTGTGTTTTATGNA 715   |
| QY | 795   | TCAAGTTTCTTTGTACAAACAAAAGGATTTGGTTGGGTGATGTGCAATGATGAGTTTCCAG 854    |

CC including coating, composites, adhesives and plasticizers. The present  
CC sequence is the Crepis palastina epoxysenase cDNA. Note: The present  
CC sequence is described as SEQ ID NO:10 in the sequence listing. But SEQ ID  
CC NO:12 on the page 2 of the specification.

XX  
SQ Sequence 1344 BP; 344 A; 308 C; 278 G; 414 T; 0 U; 0 Other;

Query Match 45.5%; Score 640.4; DB 14; Length 1344;  
Best Local Similarity 75.5%; Pred. No. 7.3e-149;  
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGGATTCGCGCGCCATTCTCGTTAAAGTATCTAAAGAAAGCAATCCCT 196  
DB 75 GAACGTGTCTCAGTTGATCCAGTAACCTTCTCACTGAGTGAATTGAAGCAAGCAATCCCT 134  
QY 197 GCACATTGCTTCCGCGCATCGCGCTCTGGTCACTCTGCTACGTAGTTACAGATCTCAAT 256  
DB 135 CCCATTGCTTCCAGAGATCTGTAATCGCTCATCTTACTATGTGTTCAAGATCTCAAT 194  
QY 257 ATCACCCTTCTTTATACACGGTGGCGAAGCACTACATTCCTCAGCTCCCTCCCTCCTA 316  
DB 195 ATTGCCTACATCTTCTACTTCTTCCCAACACATATATCCCTACTCTTCCCTACTAGTCTA 254  
QY 317 GTTACTTAGCATGCGCGTTTACTGTTTGGCAATCTTGCATCTCTCACTGGTTTATGG 376  
DB 255 GCCTACTTAGCTTGGCCCGTTTACTGGTTCGTCAAGCTAGGCTCTCCTCAGCTTATGG 314  
QY 377 GTCTCTGGCCATGAATCGGCGCATCATGCTTTAGTGTAGTACCAGTGGATTGATAACGCC 436  
DB 315 ATCTCGGCCCAAGATGGTCAACATGCTTTAGCACTACACATGGTTTGACGACACT 374  
QY 437 GTTGAATTCGCTCCATTCGGCTCTCTCAACCTTACTTCTTGGAAATACAGCCAT 496  
DB 375 GTGGCTTCATCTCCACTCATTTCTCCTCAACCGGTATTTCTCTTGGAAATTCAGTCAC 434  
QY 497 CGAAGACACCATGCAACACAAATTCCTCGAAGACAGGAGTTTACATTCCTAGAACT 556  
DB 435 CGGAATACCAATTCGACACAAAGTTTCGATTGATACGATGAAGTTTACATTCGGAAGAC 494  
QY 557 CAGTCCCAAGCTCAGGACTTACTCCACATACGAATTTCTTGACACACACCGCTGGTCGAATC 616  
DB 495 AAGTCCAAACTCGCGGT- ----ATCTATAAATCTTTAACAACCCACCTGGTCGGCTG 548  
QY 617 CTCATCTTTGGTCATCATGTTAACTTAGGATTTCTCTTATACCTCTTAAAGAAATGTTCA 676  
DB 549 TTGGTTTGAATATCATGTTCAACCTTAGGATTTCTCTTATACCTCTTGACAAATATTTCC 608  
QY 677 GGCAGAAGTAGATAGATTTACCAACCATTTGATCCATTGAGCCCGATCTTCACCGAG 736  
DB 609 GGCAGAAGTAGAGAGGTTTGGCAACCATCTCGACCCCATGAGTCCAAATTTCAAAGAA 668  
QY 737 COTGAGCGAATCCAGTTGCGTTATCAGATCTTGGTATCGTTGTCAGTGTGTTTACCGACTC 796  
DB 669 CGTGAGCGGTTTCAGGTTCTCTCTTTCCGATCTTGGTCTTCTTGGCGGTGTTTATGGAAT 728  
QY 797 AAGTTTCTTGTAACAAAGGATTTGGTGGGTGATGTGATGTATGGAGTTCAGTG 856  
DB 729 AAGTTGCTGTAGCAAAATAAGGAGCTGTTGGGTAGCGTGCATGTATGGAGTTCGGTA 788  
QY 857 ATAGGTCTGAATTCCTTCAATTCATTAATCTGATCTGACCAACACATCTGTCGTCA 916  
DB 789 TTAGGCGGATTTTACCTTTTTCGATGTGATCACCTTCTTGACCAACCCATCAGTCGTG 848  
QY 917 CCCCAATTACGAATCAACCGAATGGAACTGGATCAAGAGGCGCTTGACCAATCGACAGA 976  
DB 849 CCTCATTTATGATTAACATGAATGGAATGGATCAGAGGGGCTTCTGACGAATCGATAGG 908  
QY 977 GATTTCCGCTCTCTGAATCGGGTTTCCACGAGTTTACACACCCAGCTGTGTCACCAT 1036  
DB 909 GACTTTGGATTTCTGAAATAGTGTGTTTCCATGATGTTTACACACACTCATGTATGTCAT 968  
QY 1037 TTGTTTCCCTCATTTCCCAATTCATTCGAAAGGAGGCAAGCGAGGCCATCAAGCCAATC 1096

DB 969 TTGTTTTTCATACATTCACACTATCATGCAAGGAGGCAAGGATGCAATCAAGCCAATC 1028  
QY 1097 TTGGGTGATTACAGGATGATCGACAGGACTCCATTTTCAAAGCAATGTGGAGAGGCC 1156  
DB 1029 TTGGGCGACTTTTATATGATCGACAGGACTCCAAATTTTAAAGCAATGTGGAGAGGGC 1088  
QY 1157 AAGGAATGCATTTTACATCGAGCAAGATGCGACAGCAAGGACACATATTGGTAC 1216  
DB 1089 AGGAGTGCATGTACATCGAGC-----CTGATAGCAAGCTCAAGGTGTTTATTGGTAT 1142  
QY 1217 CATAAAATGTAATC 1230  
DB 1143 CATAAATTTGATC 1156

Search completed: September 25, 2006, 00:17:02  
Job time : 1366 secs

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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:55:37 ; Search time 183 Seconds  
(without alignments)  
956.804 Million cell updates/sec

Title: US-10-622-774-2

Perfect score: 2086  
Sequence: 1 MSDSYDDRMKDHMDERAPI.....IYIEQDADSKHKGTWYHKM 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:\*  
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5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 2086   | 100.0       | 378    | 5  | US-10-622-774-2    |
| 2          | 2077   | 99.6        | 378    | 5  | US-10-912-534-136  |
| 3          | 1549.5 | 74.3        | 377    | 4  | US-10-772-227-36   |
| 4          | 1549.5 | 74.3        | 377    | 4  | US-10-772-227-38   |
| 5          | 1549.5 | 74.3        | 377    | 4  | US-10-772-227-42   |
| 6          | 1549.5 | 74.3        | 377    | 5  | US-10-912-534-36   |
| 7          | 1549.5 | 74.3        | 377    | 5  | US-10-912-534-38   |
| 8          | 1549.5 | 74.3        | 377    | 5  | US-10-912-534-42   |
| 9          | 1523.5 | 73.0        | 377    | 5  | US-10-732-923-4878 |
| 10         | 1504   | 72.1        | 374    | 4  | US-10-772-227-41   |
| 11         | 1504   | 72.1        | 374    | 5  | US-10-912-534-41   |
| 12         | 1501   | 72.0        | 373    | 3  | US-09-981-124-41   |
| 13         | 1499   | 71.9        | 374    | 5  | US-10-912-534-137  |
| 14         | 1498   | 71.8        | 374    | 5  | US-10-772-227-18   |
| 15         | 1498   | 71.8        | 374    | 5  | US-10-912-534-18   |
| 16         | 1497   | 71.8        | 374    | 5  | US-10-912-534-135  |
| 17         | 1493   | 71.6        | 374    | 3  | US-09-981-124-2    |
| 18         | 1493   | 71.6        | 374    | 5  | US-10-732-923-4887 |
| 19         | 1482   | 71.0        | 380    | 4  | US-10-772-227-24   |
| 20         | 1482   | 71.0        | 380    | 5  | US-10-912-534-24   |
| 21         | 1424.5 | 68.3        | 375    | 5  | US-10-732-923-4836 |
| 22         | 1410   | 67.6        | 326    | 6  | US-11-087-099-3460 |
| 23         | 1386   | 66.4        | 384    | 3  | US-09-981-124-20   |
| 24         | 1351   | 64.8        | 326    | 6  | US-11-087-099-6724 |
| 25         | 1290.5 | 61.9        | 383    | 5  | US-10-732-923-4841 |
| 26         | 1284.5 | 61.6        | 383    | 5  | US-10-732-923-4840 |
| 27         | 1279   | 61.3        | 383    | 4  | US-10-464-631-15   |

ALIGNMENTS

RESULT 1

US-10-622-774-2

; Sequence 2, Application US/10622774  
; Publication NO. US2005002270A1

; GENERAL INFORMATION:

; APPLICANT: University of Kentucky Research Foundation

; APPLICANT: Hildebrand, David

; APPLICANT: Hatanaka, Tomoko

; TITLE OF INVENTION: RECOMBINANT STOKESIA EPSYGENASE GENE

; FILE REFERENCE: 050229-0377

; CURRENT APPLICATION NUMBER: US/10/622,774

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: 60/396,406

; PRIOR FILING DATE: 2002-07-19

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Stokesia laevis

US-10-622-774-2

Query Match 100.0%; Score 2086; DB 5; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.7e-197;

Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSYDDRMKDHMDERAPIIDPAPFSLDLKKAIPAHCFFRSAAVMSSCYVVDLIITFLL 60

DB 1 MSDSYDDRMKDHMDERAPIIDPAPFSLDLKKAIPAHCFFRSAAVMSSCYVVDLIITFLL 60

QY 61 YTVANTYIPLHPPLVYLAWPYVWCQSCILGLWLHCEGCHHAFSEYQWIDNAGFVL 120

DB 61 YTVANTYIPLHPPLVYLAWPYVWCQSCILGLWLHCEGCHHAFSEYQWIDNAGFVL 120

QY 121 HSALTPTPSWKYSHRKHANTNSLENEBVIPTQSQRLTYSTYFELDNTPGRIILVI 180

DB 121 HSALTPTPSWKYSHRKHANTNSLENEBVIPTQSQRLTYSTYFELDNTPGRIILVI 180

QY 181 MLTGLFPPLYLLTNVSGKKYDRFTNHFDPISPFTERRERIQVALSDLGIVAVFYGLKFLVQ 240

DB 181 MLTGLFPPLYLLTNVSGKKYDRFTNHFDPISPFTERRERIQVALSDLGIVAVFYGLKFLVQ 240

QY 241 TKGFGWCMYGVPIGLNSFIIVITLYLHHTLSSPHYDSTENWIKGALTIDRDFGLL 300

DB 241 TKGFGWCMYGVPIGLNSFIIVITLYLHHTLSSPHYDSTENWIKGALTIDRDFGLL 300

QY 301 NEVFDHVTHTVHLHLPVYIPHYHAKASEAKPIILGDYRMDRTPPPFKAMWEAKECIY 360

DB 301 NEVFDHVTHTVHLHLPVYIPHYHAKASEAKPIILGDYRMDRTPPPFKAMWEAKECIY 360

Qy 361 IEQDADSKHGKTYWYHKM 378  
Db 361 IEQDADSKHGKTYWYHKM 378

## RESULT 2

US-10-912-534-136  
; Sequence 136, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbesky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Deryck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: US 10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 136  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Stokesia laevis B  
US-10-912-534-136

Query Match 99.6%; Score 2077; DB 5; Length 378;  
Best Local Similarity 99.5%; Pred. No. 1.3e-196;  
Matches 376; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDSVDDRMKDHMDERAPIDPAPPSLSDLKKAIPAHCFFRSAYVSSCVVQDLIIITFL 60  
Db 1 MASSYDDRMKDHMDERAPIDPAPPSLSDLKKAIPAHCFFRSAYVSSCVVQDLIIITFL 60  
Qy 61 YTVANTYIPLPPLVYLAWPVYWFQSCILTLGLWLGHECGHAFSEYQWIDNAGFVL 120  
Db 61 YTVANTYIPLPPLVYLAWPVYWFQSCILTLGLWLGHECGHAFSEYQWIDNAGFVL 120  
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEBEVYIPRTQSQLRTYSTYEFLDNTPGRLILVI 180  
Db 121 HSALLTPYFSWKYSHRKHANTNSLENEBEVYIPRTQSQLRTYSTYEFLDNTPGRLILVI 180  
Qy 181 MLTLGFPYLLTNVSGKGYDRFTNHFDPDSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240  
Db 181 MLTLGFPYLLTNVSGKGYDRFTNHFDPDSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240  
Qy 241 TKGFGVWCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTEWNIKGALTITIDRDFGLL 300  
Db 241 TKGFGVWCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTEWNIKGALTITIDRDFGLL 300  
Qy 301 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 360  
Db 301 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 360  
Qy 361 IEQDADSKHGKTYWYHKM 378  
Db 361 IEQDADSKHGKTYWYHKM 378

## RESULT 3

US-10-772-227-36  
; Sequence 36, Application US/10772227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbesky, Michelle L.  
; APPLICANT: Baublite, Catherine

; APPLICANT: Williams, Deryck J.  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Stokesia laevis  
US-10-772-227-36

Query Match 74.3%; Score 1549.5; DB 4; Length 377;  
Best Local Similarity 72.0%; Pred. No. 2.2e-144;  
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSVDDRMKDHMDERAPIDPAPPSLSDLKKAIPAHCFFRSAYVSSCVVQDLIIITFL 60  
Db 7 MSDLSGDK----NLKRVFVDP--PFTLSDIKKAIPPHCFKRSVIRSSYYVVDHLIVSYVF 61  
Qy 61 YTVANTYIPLPPLVYLAWPVYWFQSCILTLGLWLGHECGHAFSEYQWIDNAGFVL 120  
Db 62 FFLATTYITVLPAPLAYIAMPVYWFQASILTGLWVIGHECGHAFSEYQWIDDTVGFL 121  
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEBEVYIPRTQSQLRTYSTYEFLDNTPGRLILVI 180  
Db 122 HSALLTPYFSWKYSHRKHANTNSLENEBEVYIPRTQSQLRTYSTYEFLDNTPGRLILVI 180  
Qy 181 MLTLGFPYLLTNVSGKGYDRFTNHFDPDSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240  
Db 180 RLTLGFPYLLTNVSGKGYDRFTNHFDPDSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 239  
Qy 241 TKGFGVWCMYGVPIGLNSFIIVTYLHHTLSSPHYDSTEWNIKGALTITIDRDFGLL 300  
Db 240 AKGAVWVTCIYGVPIGLNSFIIVTYLHHTLSSPHYDSTEWNIKGALTITIDRDFGLL 299  
Qy 301 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 360  
Db 300 NRVFHDVTHVHLHLPFYIPHYHAKSEAKIPILGDYRMDIRTPPFKAMWREAKECIY 359  
Qy 361 IEQDADSKHGKTYWYHKM 378  
Db 360 IEQDADSKHGKTYWYHKM 377

## RESULT 4

US-10-772-227-38  
; Sequence 38, Application US/10772227  
; Publication No. US20040168213A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbesky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Williams, Deryck J.  
; APPLICANT: Kloek, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC  
; FILE REFERENCE: 12557-016001  
; CURRENT APPLICATION NUMBER: US/10/772,227  
; CURRENT FILING DATE: 2004-02-04  
; PRIOR APPLICATION NUMBER: US 60/445,293  
; PRIOR FILING DATE: 2003-02-05  
; NUMBER OF SEQ ID NOS: 130



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Db 180 RLTLGFPPLLTNTISGKKYQRPANHPDPLSPFTTERERIQVLVSDGLLAVIYAIKLLVA 239
Qy 241 TKFGWVMCMYGPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300
Db 240 AKGAVWTCIYGPVIGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299
Qy 301 NRVPDVTHTVHLHLLFPYIPHYHAKSEAIKPLGDYRMDTRTPPFKAMWREAKECIY 360
Db 300 NRVPDVTHTVHLHLLISYIPHYHAKSEAIKPLVDYIKIDRTPPIFKAMWREAKECIY 359
Qy 361 IEQADSKHKGYWYHKM 378
Db 360 IEPDEDTEHKGYYWYHKM 377

RESULT 7
US-10-912-534-38
; Sequence 38, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Williams, Rodolfo
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Stokesia laevis
US-10-912-534-38

Query Match 74.3%; Score 1549.5; DB 5; Length 377;
Best Local Similarity 72.0%; Pred. No. 2.2e-144;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSDK-----NLKRVDPDP--PFTLSDIKKAIKPAHCFRRSAVWSSCVVQDLITPFL 60
Db 7 MSDSDK-----NLKRVDPDP--PFTLSDIKKAIKPAHCFRRSAVWSSCVVQDLITPFL 61
Qy 61 YTVANTYIPLPPLVYLAWPVYFQCSCILTLGLVWLGHECGHAFSEYQWIDNAGFVL 120
Db 62 PFLATTYITVLPAPLAYIAMPVYFQCSCILTLGLVWLGHECGHAFSEYQWIDNAGFVL 121
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTVEFLDNTPGRLILVI 180
Db 122 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTVEFLDNTPGRLILVI 179
Qy 181 MLTLGFPPLLTNTISGKKYQRPANHPDPLSPFTTERERIQVALSDGLIYAVFYGLKFLVQ 240
Db 180 RLTLGFPPLLTNTISGKKYQRPANHPDPLSPFTTERERIQVLVSDGLLAVIYAIKLLVA 239
Qy 241 TKFGWVMCMYGPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300
Db 240 AKGAVWTCIYGPVIGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299
Qy 301 NRVPDVTHTVHLHLLFPYIPHYHAKSEAIKPLGDYRMDTRTPPFKAMWREAKECIY 360
Db 300 NRVPDVTHTVHLHLLISYIPHYHAKSEAIKPLVDYIKIDRTPPIFKAMWREAKECIY 359
Qy 361 IEQADSKHKGYWYHKM 378
Db 360 IEPDEDTEHKGYYWYHKM 377

RESULT 9
US-10-923-923-4878
; Sequence 4878, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
```

```
Db 360 IEPDEDTEHKGYYWYHKM 377

RESULT 8
US-10-912-534-42
; Sequence 42, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Williams, Rodolfo
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Stokesia laevis
US-10-912-534-42

Query Match 74.3%; Score 1549.5; DB 5; Length 377;
Best Local Similarity 72.0%; Pred. No. 2.2e-144;
Matches 272; Conservative 47; Mismatches 52; Indels 7; Gaps 3;

Qy 1 MSDSDK-----NLKRVDPDP--PFTLSDIKKAIKPAHCFRRSAVWSSCVVQDLITPFL 60
Db 7 MSDSDK-----NLKRVDPDP--PFTLSDIKKAIKPAHCFRRSAVWSSCVVQDLITPFL 61
Qy 61 YTVANTYIPLPPLVYLAWPVYFQCSCILTLGLVWLGHECGHAFSEYQWIDNAGFVL 120
Db 62 PFLATTYITVLPAPLAYIAMPVYFQCSCILTLGLVWLGHECGHAFSEYQWIDNAGFVL 121
Qy 121 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTVEFLDNTPGRLILVI 180
Db 122 HSALLTPYFSWKYSHRKHANTNSLENEEVIPTQSQLRTYSTVEFLDNTPGRLILVI 179
Qy 181 MLTLGFPPLLTNTISGKKYQRPANHPDPLSPFTTERERIQVALSDGLIYAVFYGLKFLVQ 240
Db 180 RLTLGFPPLLTNTISGKKYQRPANHPDPLSPFTTERERIQVLVSDGLLAVIYAIKLLVA 239
Qy 241 TKFGWVMCMYGPVIGLNSFIIVITYLHHTLSSPHYDSTENWIKGALTITDRDFGLL 300
Db 240 AKGAVWTCIYGPVIGVSVFVLITYLHHTLSPHYDSTENWIRGALSTIDRDFGL 299
Qy 301 NRVPDVTHTVHLHLLFPYIPHYHAKSEAIKPLGDYRMDTRTPPFKAMWREAKECIY 360
Db 300 NRVPDVTHTVHLHLLISYIPHYHAKSEAIKPLVDYIKIDRTPPIFKAMWREAKECIY 359
Qy 361 IEQADSKHKGYWYHKM 378
Db 360 IEPDEDTEHKGYYWYHKM 377

RESULT 9
US-10-923-923-4878
; Sequence 4878, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
```

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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 4878
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Calendula officinalis
US-10-732-923-4878

Query Match
Best Local Similarity 73.0%; Score 1523.5; DB 5; Length 377;
Matches 261; Conservative 45; Mismatches 54; Indels 7; Gaps 3;

QY 8 RMDK----HMDERAPIDPAPFSLDLKKAIPAHCFFRSVAVWSSCVVQDLIIITFLYTV 63
DB 6 RNSDPSEGNILERVDPDP-PTLSDLKKAIPHCFFRSVIRSSYYVVDLIIAYVFFYL 64
QY 64 ANTYIPLPPPLVYLAWPVWFCQSCILTGLMWLHCEGCHHAFSEYQWIDNNAVGFLV 123
DB 65 ANTYIPLPTPLAYLAWPVWFCQASILTGLMWLHCEGCHHAFSDYQLDIDIVGFV 124
QY 124 ILTPFESWKYSHRKHANTNSLENEEVYIPRTQSQLRTYSTYFEFLDNTGRILILV 183
DB 125 LUTPFESWKYSHRKHANTNSLNDDEVYIPKRSKVIYS--KLLNPPGRVFTLFR 182
QY 184 LGFPLLLTNVSGKYDRFTNHPDPLSPFTTEREQVALSDLGIVAVFYGLKFLVOT 243
DB 183 LGFPLLLTNISGKYGRFANHPDPSPIFNDRERVQVLSDFGLLAIFYAKLLVA 242
QY 244 FGVMCMYGVVIGLNSPIIVITYLHHTLSSPHYDSTENWIKGALTTIDRDFGL 303
DB 243 AAWVINMYAIPVLGVSVFFVLLTYLHHTLSSPHYDSTENWIKGALSTIDR 302
QY 304 FHDVTHVHLHLPYIPHYHAKSEAIKPILDYRMDTRDTPPFKAMWREAKEC 363
DB 303 FHDVTHVHLHLISYIPHYHAKARDAIKPVLGEYIKIDRTPIPKAMYREAKE 362
QY 364 DADSKHKGYWYVHKM 378
DB 363 DEDSEHKGVFWYHKM 377

RESULT 10
US-10-772-227-41
; Sequence 41, Application US/10772227
; Publication No. US20040168213A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Williams, Deryck J.
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772,227
; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; PRIOR FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
US-10-772-227-41

Query Match
Best Local Similarity 72.1%; Score 1504; DB 4; Length 374;
Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

QY 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFFRSVAVWSSCVVQDLIIITFL 60
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKQAIPPHCFORSVIRSSYYVVDLIIAYIF 60
QY 61 YTVANTYIPLPPPLVYLAWPVWFCQSCILTGLMWLHCEGCHHAFSEYQWIDNNAVG 120
DB 61 YFLADKYIPIPLAPLAYLAWPVWFCQASILTGLMWLHCEGCHHAFSEYQWVD 120
QY 121 HSALLTPFESWKYSHRKHANTNSLENEEVYIPRTQSQLRTYSTYFEFLDNTGRIL 180
DB 121 HSFLTPFESWKYSHRKHANTSSINDDEVYIPKSKLAL--TYKLLNPPGRLLVMI 178
QY 181 MLTGLFPPLVLLTNVSGKYDRFTNHPDPLSPFTTEREQVALSDLGIVAVFYGLKFL 240
DB 179 MFTLGFPLVLLTNISGKYDRFANHPDPSPIFKERERFQVLLSDGLLAVFGIKVA 238
QY 241 TKGFQWCMYGVVIGLNSPIIVITYLHHTLSSPHYDSTENWIKGALTTIDRDFGL 300
DB 239 KKGAAWVACMYGVPMGLGVFTFDIITYLHHTHQSPPHYDSTENWIRGALSIDRDF 298
QY 301 NRVFHDVTHVHLHLPYIPHYHAKSEAIKPILDYRMDTRDTPPFKAMWREAKEC 360
DB 299 NSVFHDVTHVTHVMHMFYIPHYHAKARDAINTIIGDYIMIDRTPIPKALWREAKE 358
QY 361 IEODADSKHKGYWYVHKM 378
DB 359 IE--PDSKRGVYVTHKL 374

RESULT 11
US-10-912-534-41
; Sequence 41, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloek, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; TITLE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hypothetical sequence
US-10-912-534-41

Query Match
Best Local Similarity 72.1%; Score 1504; DB 5; Length 374;
Matches 261; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

QY 1 MSDSYDDRMKDHMDERAPIDPAPFSLDLKKAIPAHCFFRSVAVWSSCVVQDLIIITFL 60
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKQAIPPHCFORSVIRSSYYVVDLIIAYIF 60
QY 61 YTVANTYIPLPPPLVYLAWPVWFCQSCILTGLMWLHCEGCHHAFSEYQWIDNNAVG 120
DB 61 YFLADKYIPIPLAPLAYLAWPVWFCQASILTGLMWLHCEGCHHAFSEYQWVD 120
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QY 121 HSALLTPFSWKYSRKHANTNSLENEVEYIPRTQSQRYSYTFEFLDNTFGRILLIIV 180  
DB 121 HSFLLTPTFSWKYSRHNHANTSSIDNDEVIPKSKSLAL--TYKLLNPPGRLLVMVI 178  
QY 181 MLTGLFPYLLTNVSGKYDRFTNHPDPLSPIFETERERIOVALSDLGIVAVFYGLKFLVQ 240  
DB 179 MFTLGFPLYLNTNISGKYDRFANHPDPMSPIFKERERFVLLSDGLLAVFYGLIKVAVA 238  
QY 241 TKGFQWVMCMYGVPIGLNSFIIVITYLHTLSSPHYDSTENWIKGALTITIDRDFGLL 300  
DB 239 KGAAWACVMYGVPMGVFTLFDIITYLHTHQSPPHYDSTENWIRGALSADRDPM 298  
QY 301 NRVDHVDVTHVHLHPYIPHYHAKESBAIKPILGDYRMDRTPFFKAMWREAKECIY 360  
DB 299 NSVFDHVDVTHVHMFMFSYIPHYHAKESDAINTIIGDYMDRTPILKALWREAKECMY 358  
QY 361 IEQDADSKHKGTWYVHKM 378  
DB 359 IE--PDSKRKGVYVYHKL 374

RESULT 12 \*  
US-09-981-124-4  
; Sequence 4, Application US/09981124  
; Patent No. US20020166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Marit  
; APPLICANT: Stymne, Sten  
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
; FILE REFERENCE: 26-98A  
; CURRENT APPLICATION NUMBER: US/09/981,124  
; PRIOR FILING DATE: 2001-10-17  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/043706  
; PRIOR FILING DATE: 1997-04-16  
; PRIOR APPLICATION NUMBER: AU P06223  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR APPLICATION NUMBER: AU P06226  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR APPLICATION NUMBER: US 60/050403  
; PRIOR FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Crepis sp.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (292)..(292)  
; OTHER INFORMATION: The 'Xaa' at location 292 stands for Arg, or Ser.  
; NAME/KEY: misc\_feature  
; LOCATION: (937)..(937)  
; OTHER INFORMATION: N is any nucleotide residue  
; NAME/KEY: misc\_feature  
; LOCATION: (901)..(901)  
; OTHER INFORMATION: N is any nucleotide residue  
US-09-981-124-4

Query Match 72.0%; Score 1501; DB 3; Length 373;  
Best Local Similarity 71.3%; Pred. No. 1.4e-139;  
Matches 259; Conservative 48; Mismatches 52; Indels 4; Gaps 2;  
QY 16 ERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFLTYVANTYIPHLPPPL 75  
DB 15 ERVSDVPTFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFLTYVANTYIPHLPPPL 74  
QY 76 VYLANPVYVFCQSCILTGLVWLGHECGHAPSEYQWIDNAVGVFLHSALLTPFSWKYS 135

DB 75 AYLANPVYVFCQSCILTGLVWLGHECGHAYSNWTWDDTVGFIHSHFLLTPFESWKYS 134  
QY 136 RKHANTNSLENEVEYIPRTQSQRYSYTFEFLDNTFGRILLIIVMLTGLPPLYLNTVS 195  
DB 135 RNHSNTSSIDNDEVIPKSKSLK--RIYKLLNPPGRLLVLMFTLGPPLYLNTNIS 192  
QY 196 GKXYDRTNHPDPLSPIFETERERIOVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGV 255  
DB 193 GKXYDRFANHPDPMSPIFKERERFVLLSDGLLAVFYGLIKVAVANKGAAMVACMYGV 252  
QY 256 IGLNSFIIVITYLHTLSSPHYDSTENWIKGALTITIDRDFGLLRNVFHDVTHVHLH 315  
DB 253 LGVTFDFVITFLHTHQSPPHYDSTENWIRGALSALDXDFGLNSVFDVTHVHMH 312  
QY 316 LFPYIPHYHAKESBAIKPILGDYRMDRTPFFKAMWREAKECIYIEODASKHKGTWY 375  
DB 313 LFSYIPHYHAKESDAIKPILGDYRMDRTPILKAMWREAGRECMYIE--PDSKLGKVYV 370  
QY 376 HKM 378  
DB 371 HKL 373

RESULT 13  
US-10-912-534-137  
; Sequence 137, Application US/10912534  
; Publication No. US20050172358A1  
; GENERAL INFORMATION:  
; APPLICANT: Verbeky, Michelle L.  
; APPLICANT: Baublite, Catherine  
; APPLICANT: Kloeck, Andrew P.  
; APPLICANT: Davila-Aponte, Jennifer A.  
; APPLICANT: Hresko, Michelle Coutu  
; APPLICANT: McLaird, Merry B.  
; APPLICANT: Zentella, Rodolfo  
; APPLICANT: Williams, Desyck J.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND  
; FILE REFERENCE: 12557-023001  
; CURRENT APPLICATION NUMBER: US/10/912,534  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: US 10/772,227  
; PRIOR FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 137  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Crepis biennis  
US-10-912-534-137

Query Match 71.9%; Score 1499; DB 5; Length 374;  
Best Local Similarity 68.8%; Pred. No. 2.2e-139;  
Matches 260; Conservative 51; Mismatches 63; Indels 4; Gaps 2;  
QY 1 MSDSYDDRMKDMDERAPIDPAPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFL 60  
DB 1 MASSGHSRTSKSVMERVSVDVPFSLDLKKAIPAHCFRRSAVSSCYVQDLIIITFL 60  
QY 61 YTVANTYIPHLPPPLVYLANPVYVFCQSCILTGLVWLGHECGHAPSEYQWIDNAVGV 120  
DB 61 YFLADKYIIPILPAPLAYLANPVYVFCQASIIITGLWILGHECGHAPSEYQWIDNAV 120  
QY 121 HSALLTPFSWKYSRKHANTNSLENEVEYIPRTQSQRYSYTFEFLDNTFGRILLIIV 180  
DB 121 HSFLLTPTFSWKYSRHNHANTSSIDNDEVIPKSKSLAL--TYKLLNPPGRLLVMVI 178  
QY 181 MLTGLFPYLLTNVSGKYDRFTNHPDPLSPIFETERERIOVALSDLGIVAVFYGLKFLVQ 240  
DB 179 MFTLGFPLYLNTNISGKYDRFANHPDPMSPIFKERERFVLLSDGLLAVFYGLIKVAVA 238  
QY 241 TKGFQWVMCMYGVPIGLNSFIIVITYLHTLSSPHYDSTENWIKGALTITIDRDFGLL 300



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Db 239 KKGAAWVACWGVGMLGVFTLFDIITLHHTHOSPHYDSTWNNWIRGALSADRDGFM 298
Qy 301 NRVEFHDVTHVHLHLPYIPHYHAKSEAIKPIIGDYRMDIDRTPPFKAMWREACECY 360
Db 299 NSVEFHDVTHVHWHMFSPIPHYHAKSEAIKPIIGDYRMDIDRTPPFKAMWREACECY 358
Qy 361 IEQDADSKHGKGYWYHKM 378
Db 359 IE--PDSKRKGWYWKHL 374
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## RESULT 14

```
US-10-772-227-18
; Sequence 18, Application US/1077227
; Publication No. US20040168213A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Williams, Deryck J.
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
; TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-016001
; CURRENT APPLICATION NUMBER: US/10/772,227
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,293
; PRIOR FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Crepis biennis
US-10-772-227-18
```

```
Query Match 71.8%; Score 1498; DB 4; Length 374;
Best Local Similarity 71.1%; Pred. No. 2.7e-139;
Matches 258; Conservative 48; Mismatches 53; Indels 4; Gaps 2;

Qy 16 ERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDLIITFLTYTANTYIPIHLPPL 75
Db 16 ERVSDVPVPSLSDLKQAIPPHCFQSRVRSYVVDLIIAIFYFLADKYPILPAFL 75
Qy 76 VYLAWPVWFQSCILTLGLWILGHCCHAFSEYQWIDNAVGVLSALLTPYFSWKYSH 135
Db 76 AYLAWPVWFQSCILTLGLWILGHCCHAFSEYQWIDNAVGVLSALLTPYFSWKYSH 135
Qy 136 RKHANTNSLENEEVIPTQSLRTYSTYFELDNTPGRIILIVIMLTGLGFLYLLTNVS 195
Db 136 RNHANTSSIDNDEVIPKSKLAL--TYKLLNPPGRLVNMVIMFTLGFPLLYLTNIS 193
Qy 196 GKDYDRFTNHFDPLSPIFTERERIOVALSDLGIVAVFYGLKFLVQTKGFWNVMYGV 255
Db 194 GKDYDRFANHFDPMSPIFKERERFQVLLSDGLLAVFYGIKVAVAKGAACVACMYGV 253
Qy 256 IGLNSFIIVITLYLHHTHSSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 315
Db 254 LGVFTLFDIITLYLHHTHOSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 313
Qy 316 LFPYIPHYHAKSEAIKPIIGDYRMDIDRTPPFKAMWREACECYIEQDADSKHGKGY 375
Db 314 MFSYIPHYHAKSEAIKPIIGDYRMDIDRTPPFKAMWREACECYIE--PDSKRKGWY 371
Qy 376 HKM 378
Db 372 HKL 374
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## RESULT 15

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US-10-912-534-18
; Sequence 18, Application US/10912534
; Publication No. US20050172358A1
; GENERAL INFORMATION:
; APPLICANT: Verbsky, Michelle L.
; APPLICANT: Baublite, Catherine
; APPLICANT: Kloeck, Andrew P.
; APPLICANT: Davila-Aponte, Jennifer A.
; APPLICANT: Hresko, Michelle Coutu
; APPLICANT: McLaird, Merry B.
; APPLICANT: Zentella, Rodolfo
; APPLICANT: Williams, Deryck J.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
; TITLE OF INVENTION: PLANTS MADE THEREFROM
; FILE REFERENCE: 12557-023001
; CURRENT APPLICATION NUMBER: US/10/912,534
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 10/772,227
; PRIOR FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Crepis biennis
US-10-912-534-18
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```
Query Match 71.8%; Score 1498; DB 5; Length 374;
Best Local Similarity 71.1%; Pred. No. 2.7e-139;
Matches 258; Conservative 48; Mismatches 53; Indels 4; Gaps 2;

Qy 16 ERAPIDPAPFSLDLKKAIPAHCFRRSAVWSSCYVQDLIITFLTYTANTYIPIHLPPL 75
Db 16 ERVSDVPVPSLSDLKQAIPPHCFQSRVRSYVVDLIIAIFYFLADKYPILPAFL 75
Qy 76 VYLAWPVWFQSCILTLGLWILGHCCHAFSEYQWIDNAVGVLSALLTPYFSWKYSH 135
Db 76 AYLAWPVWFQSCILTLGLWILGHCCHAFSEYQWIDNAVGVLSALLTPYFSWKYSH 135
Qy 136 RKHANTNSLENEEVIPTQSLRTYSTYFELDNTPGRIILIVIMLTGLGFLYLLTNVS 195
Db 136 RNHANTSSIDNDEVIPKSKLAL--TYKLLNPPGRLVNMVIMFTLGFPLLYLTNIS 193
Qy 196 GKDYDRFTNHFDPLSPIFTERERIOVALSDLGIVAVFYGLKFLVQTKGFWNVMYGV 255
Db 194 GKDYDRFANHFDPMSPIFKERERFQVLLSDGLLAVFYGIKVAVAKGAACVACMYGV 253
Qy 256 IGLNSFIIVITLYLHHTHSSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 315
Db 254 LGVFTLFDIITLYLHHTHOSPHYDSTWNNWIRGALSADRDGFMNSVFDVTHVHMH 313
Qy 316 LFPYIPHYHAKSEAIKPIIGDYRMDIDRTPPFKAMWREACECYIEQDADSKHGKGY 375
Db 314 MFSYIPHYHAKSEAIKPIIGDYRMDIDRTPPFKAMWREACECYIE--PDSKRKGWY 371
Qy 376 HKM 378
Db 372 HKL 374
```

Search completed: September 22, 2006, 19:59:18  
Job time : 184 secs

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| Result No. | Query | Score | Match |   | Length   | DB                 | ID | Description |
|------------|-------|-------|-------|---|----------|--------------------|----|-------------|
|            |       |       |       | % |          |                    |    |             |
| 1          | 1406  | 100.0 | 1406  | 4 | AY462108 | Stokesia           |    |             |
| 2          | 870   | 61.9  | 1364  | 4 | AR064128 | Sequence           |    |             |
| 3          | 673   | 47.9  | 1152  | 4 | CP245938 | Calendula          |    |             |
| 4          | 673   | 47.9  | 1285  | 2 | AX089471 | Sequence           |    |             |
| 5          | 664.8 | 47.3  | 1419  | 4 | AY166773 | Helianthu          |    |             |
| 6          | 657.6 | 46.8  | 1312  | 2 | BD061165 | Plant fat          |    |             |
| 7          | 657.6 | 46.8  | 1312  | 2 | AR367438 | Sequence           |    |             |
| 8          | 657.6 | 46.8  | 1312  | 2 | AX031162 | Sequence           |    |             |
| 9          | 641.6 | 45.6  | 979   | 4 | AY166777 | Dimorphot          |    |             |
| 10         | 640.4 | 45.5  | 1358  | 2 | BD061164 | Plant fat          |    |             |
| 11         | 640.4 | 45.5  | 1358  | 2 | CS023935 | Sequence           |    |             |
| 12         | 640.4 | 45.5  | 1358  | 2 | CS023951 | Sequence           |    |             |
| 13         | 640.4 | 45.5  | 1358  | 2 | CS023971 | Sequence           |    |             |
| 14         | 640.4 | 45.5  | 1358  | 2 | AR367437 | Sequence           |    |             |
| 15         | 640.4 | 45.5  | 1358  | 2 | AX031160 | Sequence           |    |             |
| 16         | 640.4 | 45.5  | 1358  | 4 | CPY16283 | Y16283 Crepis pala |    |             |
| 17         | 612.8 | 43.6  | 1435  | 2 | CS023933 | Sequence           |    |             |
| 18         | 612.8 | 43.6  | 1435  | 2 | CS023943 | Sequence           |    |             |

|                            |     |  |      |
|----------------------------|-----|--|------|
| Query Match                |     | 100.0%; Score 1406; DB 4; Length 1406;                           |      |
| Best Local Similarity      |     | 100.0%; Pred. No. 0;   |      |
| Matches 1406; Conservative |     | 0; Mismatches 0; Indels 0; Gaps 0;                               |      |
| Qy                         | 1   | GTAGGTTTGGGTCCTCGGTGAGATCAGTGTGTCGACCGGAATCCAAACGATTTCTTAATTT    | 60   |
| Db                         | 1   | GTAGGTTTGGGTCCTCGGTGAGATCAGTGTGTCGACCGGAATCCAAACGATTTCTTAATTT    | 60   |
| Qy                         | 61  | GGATTTTCAGAAATCTGGGAGAAAGGTAGCAGAAATGTCGATTTTCATATGATGATCGAATGAA | 120  |
| Db                         | 61  | GGATTTTCAGAAATCTGGGAGAAAGGTAGCAGAAATGTCGATTTTCATATGATGATCGAATGAA | 120  |
| Qy                         | 121 | AGATCATGATATGACGAAACGAGCCCGGATGATCGCGCGCATTCCTGTTTAAGTGATCT      | 180  |
| Db                         | 121 | AGATCATGATATGACGAAACGAGCCCGGATGATCGCGCGCATTCCTGTTTAAGTGATCT      | 180  |
| Qy                         | 181 | AAAGAAAGCAATCCTCGACATTCCTTCGGCGGATCGCGCGTCTGGTCACTCCTGCTACGT     | 240  |
| Db                         | 181 | AAAGAAAGCAATCCTCGACATTCCTTCGGCGGATCGCGCGTCTGGTCACTCCTGCTACGT     | 240  |
| Qy                         | 241 | AGTTTCAGGATCTCATTAATCACTTCCTTTTATACACGTCGCCAACACCTACATTCCTCA     | 300  |
| Db                         | 241 | AGTTTCAGGATCTCATTAATCACTTCCTTTTATACACGTCGCCAACACCTACATTCCTCA     | 300  |
| Qy                         | 301 | CCTCCCTCCTCCTCTAGTTTACTTAGCATGCGCGGTTTACTGTTTTCGCAATCTTGAT       | 360  |
| Db                         | 301 | CCTCCCTCCTCCTCTAGTTTACTTAGCATGCGCGGTTTACTGTTTTCGCAATCTTGAT       | 360  |
| Qy                         | 361 | CCTCACTGGTTTATGGTTCCTCGGCCATGATCGGCCCATCGCTTTAGTGAGTACCA         | 420  |
| Db                         | 361 | CCTCACTGGTTTATGGTTCCTCGGCCATGATCGGCCCATCGCTTTAGTGAGTACCA         | 420  |
| Qy                         | 421 | GTGATTTGATAACGCGGTGGATTTCGTCTCCTCAATTCGGCTCTCCTCACCCCTTACTTTTC   | 480  |
| Db                         | 421 | GTGATTTGATAACGCGGTGGATTTCGTCTCCTCAATTCGGCTCTCCTCACCCCTTACTTTTC   | 480  |
| Qy                         | 481 | TTGAAATACAGCCATCGAAAGCCACATGCAAAACAAATTCATCTGAAACGAGGAAT         | 540  |
| Db                         | 481 | TTGAAATACAGCCATCGAAAGCCACATGCAAAACAAATTCATCTGAAACGAGGAAT         | 540  |
| Qy                         | 541 | TTATATTCCTAGACTCAGTCCAGCTCAGGACTTACTCCACATACGAAATTTCTTGACAA      | 600  |
| Db                         | 541 | TTATATTCCTAGACTCAGTCCAGCTCAGGACTTACTCCACATACGAAATTTCTTGACAA      | 600  |
| Qy                         | 601 | CACGCTGGTCCGAATCCTCATCTTGGTCACTATGTTAACCTTAGGATTTCTTTATACCT      | 660  |
| Db                         | 601 | CACGCTGGTCCGAATCCTCATCTTGGTCACTATGTTAACCTTAGGATTTCTTTATACCT      | 660  |
| Qy                         | 661 | CTTAAACGAATGTTTCAGGCAAGAGTACGATAGATTTTACCAACCACTTTGATTCATGAG     | 720  |
| Db                         | 661 | CTTAAACGAATGTTTCAGGCAAGAGTACGATAGATTTTACCAACCACTTTGATTCATGAG     | 720  |
| Qy                         | 721 | CCCGATCTTCCAGCGGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGC       | 780  |
| Db                         | 721 | CCCGATCTTCCAGCGGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGC       | 780  |
| Qy                         | 781 | AGTGTTTTACCGACTCAAGTTTCTTGTAACAAACAAAGGATTTGGTTGGGTGATGTGCAT     | 840  |
| Db                         | 781 | AGTGTTTTACCGACTCAAGTTTCTTGTAACAAACAAAGGATTTGGTTGGGTGATGTGCAT     | 840  |
| Qy                         | 841 | GATGAGGTTCCAGTGATAGTGTGAATTCCTTCATATCGTAATCACTTATCTGACCA         | 900  |
| Db                         | 841 | GATGAGGTTCCAGTGATAGTGTGAATTCCTTCATATCGTAATCACTTATCTGACCA         | 900  |
| Qy                         | 901 | CACACATCTGTCGTCACCCCATACGATTCACCGAATGGAATCGGATCAAGAGGCGCTT       | 960  |
| Db                         | 901 | CACACATCTGTCGTCACCCCATACGATTCACCGAATGGAATCGGATCAAGAGGCGCTT       | 960  |
| Qy                         | 961 | GACCACATCGACAGAGATTTCCGTTCTCCTGAAATCGGGTTTTCCACGACGTTTACACAC     | 1020 |
| Db                         | 961 | GACCACATCGACAGAGATTTCCGTTCTCCTGAAATCGGGTTTTCCACGACGTTTACACAC     | 1020 |

|                           |      |  |                            |
|---------------------------|------|--|----------------------------|
| Qy                        | 1021 | CCAGCTGTTGCACCATTTGTTTCCCTACATTTCCACATTATCATGCAAGGAGGCAAGCGA   | 1080                       |
| Db                        | 1021 | CCAGCTGTTGCACCATTTGTTTCCCTACATTTCCACATTATCATGCAAGGAGGCAAGCGA   | 1080                       |
| Qy                        | 1081 | GGCCATCAAGCCCAATCTTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCRAAGC  | 1140                       |
| Db                        | 1081 | GGCCATCAAGCCCAATCTTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCRAAGC  | 1140                       |
| Qy                        | 1141 | AATGTGGAGAGAGGCGCAAGGAATGCAATTTATCATCGAGCAAGATGCGACAGCAAGCAAA  | 1200                       |
| Db                        | 1141 | AATGTGGAGAGAGGCGCAAGGAATGCAATTTATCATCGAGCAAGATGCGACAGCAAGCAAA  | 1200                       |
| Qy                        | 1201 | AGGACATATTTGCTTACCATAAATGTAATCGATGATGGAGTTTGTGGAATAATGACA      | 1260                       |
| Db                        | 1201 | AGGACATATTTGCTTACCATAAATGTAATCGATGATGGAGTTTGTGGAATAATGACA      | 1260                       |
| Qy                        | 1261 | TGCAGCATCCTTTTGTATGCTTGAATCGTTCCTTATTTCTTATATGTTTGTGAAGTAAA    | 1320                       |
| Db                        | 1261 | TGCAGCATCCTTTTGTATGCTTGAATCGTTCCTTATTTCTTATATGTTTGTGAAGTAAA    | 1320                       |
| Qy                        | 1321 | TAAATTAATCTTTGAGTGAAGATGGGAGCAGGAAACAGCAGCAATATATACGCTAAAA     | 1380                       |
| Db                        | 1321 | TAAATTAATCTTTGAGTGAAGATGGGAGCAGGAAACAGCAGCAATATATACGCTAAAA     | 1380                       |
| Qy                        | 1381 | AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1406                              |                            |
| Db                        | 1381 | AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1406                              |                            |
| RESULT 2                  |      |  |                            |
| AR064128                  |      | 1364 bp  | DNA linear PAT 29-SEP-1999 |
| LOCUS                     |      | Sequence 3 from patent US 5846784.                             |                            |
| DEFINITION                |      | AR064128   |                            |
| ACCESSION                 |      | AR064128.1   | GI:5993436                 |
| VERSION                   |      |  |                            |
| KEYWORDS                  |      | Unknown.   |                            |
| SOURCE                    |      | Unclassified.  |                            |
| ORGANISM                  |      | Hitz, W.D.   |                            |
| REFERENCE                 |      | Fatty acid modifying enzymes from developing seeds of Vernonia |                            |
| AUTHORS                   |      | galanensis   |                            |
| TITLE                     |      | Patent: US 5846784-A 3 08-DEC-1998;                            |                            |
| JOURNAL                   |      | Location/Qualifiers  |                            |
| FEATURES                  |      | source   | 1. .1364                   |
|                           |      | /organism="unknown"  |                            |
|                           |      | /mol_type="unassigned DNA"                                     |                            |
| ORIGIN                    |      |  |                            |
| Query Match               |      | 61.9%; Score 870; DB 2; Length 1364;                           |                            |
| Best Local Similarity     |      | 86.1%; Pred. No. 6.9e-200;                                     |                            |
| Matches 963; Conservative |      | 0; Mismatches 155; Indels 0; Gaps 0;                           |                            |
| Qy                        | 120  | AAGATCATGATATGACGACGAGCCCGGATTCATCGCGCCATTCCTCGTTAAGTGATC      | 179                        |
| Db                        | 149  | ATGATCATATATAAAGCAACGACGTCACCGTTCATCGCGCCATTCCTCGTTAAGTGATC    | 208                        |
| Qy                        | 180  | TAAAGAAAGCAATCCCTGACATTCCTTCGCGCGATCCGCGTCTGGTTCATCTGTTACG     | 239                        |
| Db                        | 209  | TAAAGAAAGCAATCCCTGACATTCCTTCGCGCGATTCGCGATTCGCGTTCGTTACG       | 268                        |
| Qy                        | 240  | TAGTTACAGGATCTCATTTATCACCTTCCTTTTATACAGCGTCGCAACACCTACATTCCT   | 299                        |
| Db                        | 269  | TTGTTACAGGATCTCATTTATCACCTTCCTTTTATACAGCGTCGCAACCTCTTACATTCCT  | 328                        |
| Qy                        | 300  | ACCTCCCTCCTCCTTAGTTTACTTAGCATGGCGGTTTACTGGTTTTCGCAATCTTGCA     | 359                        |
| Db                        | 329  | TTCTTCCTCCTCCTTACCTTACTTAGCATGGCGGTTTACTGGTTTTCGCAATCTTGCA     | 388                        |
| Qy                        | 360  | TCCTCACTGGTTTATGGGTCTCCTCGGCCATGAATCGGCCCATCATGCTTTAGTGAGTACC  | 419                        |
| Db                        | 389  | TCCTCACTGGTTTATGGGTCTCCTCGGCCATGAATCGGCCCATCATGCTTTAGTGAGTACC  | 448                        |



Db 491 CCA-----AACTTCTTAACAATCCACCGCGGAGGTTCACATTTGGTGTTCGGTTGA 544  
Qy 639 CTTTAGGATTTCTTTATACCTTTAAGCAATGTTTACGGAAGAGTACGATAGATTTA 698  
Db 545 CTTTAGGATTTCCGTTATACCTTTAACTAATACTCGGGCAAGAAATACGGAGGTTG 604  
Qy 699 CCAACCACTTTGATCCATTGAGCCGGATCTTACCGAGCGTGAGCGAATCCAGGTTGGT 758  
Db 605 CCAACCACTTTGATCCCATGAGTCCCAATTTTCAACGATCGTGAACGGGTTCAAGTTTTC 664  
Qy 759 TATCAGATCTTGGTATCGTTCAGTGTGTTTACGAGCTCAAGTCTTCTGTACAAAACAAAG 818  
Db 665 TATCGATTTCCGTTCTCTCGTGTATTTATGAATCAAGCTTCTTGTAGCAGCAAAAG 724  
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Db 965 ATCATGCAAGAGGCAAGGAGTGAATCAAGCCAGTGTGCGGAGTACTATAAAATCG 1024  
Qy 1119 ACAGAGCTCCATTTTCAAGCAATGTGAGAGAGGCAAGGAATGCAATTTACATTCGAGC 1178  
Db 1025 ACAGAGCTCCATTTTCAAGCAATGTATAGAGGCTAAGGAATGCATCTACATCGAGC 1084  
Qy 1179 AAGATGCAGACGACGACAAAGGAGCATATTTGGTACCAATAAATGTAATCGATGATG 1237  
Db 1085 CCGATGAGGATAGCGAGCACAAAGGTGTCTGTCACCAAGATGTAATCAAAAGG 1143

RESULT 4  
AX089471  
LOCUS AX089471.1 1285 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 1 from Patent WO0116362.  
ACCESSION AX089471  
VERSION AX089471.1 GI:13443732  
KEYWORDS  
SOURCE  
ORGANISM  
Calendula officinalis  
Calendula officinalis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Calenduleae; Calendula.  
1  
REFERENCE  
1. Feussner, I., Hornung, E., Fritsche, K., Peitzsch, N. and Renz, A.  
Patty acid desaturase gene from plants  
Patent: WO 0116362-A 1 08-MAR-2001;  
BASF AKTIENGESSELLSCHAFT (DE)  
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Best Local Similarity 77.2%; Pred. No. 4.1e-152;  
Matches 833; Conservative 0; Mismatches 240; Indels 6; Gaps 1;  
Qy 159 CGCATTTCTCGTTAAGTGATCTAAAGAAAGCAATCCCTGCACATTTGCTTCGGGCGATCCG 218  
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Qy 219 CCGTCTGGTCATCTCGTACGTAGTTAGGATCTCAATATTCACCTTCCTTTTATACACGG 278  
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Qy 279 TCGCAACACCTACATTCCTCACCTCCCTCCTCTAGTTTACTTAGCATGCGCGGTTT 338  
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Qy 339 ACTGGTTTTCGCAATCTTGCATCTCACTGGTTTATGCGGTCTCGGCCATGAATGCGGCC 398  
Db 292 ACTGGTTTTCGCAATCTTGCATCTCACTGGTTTATGCGGTCTCGGCCATGAATGCGGCC 351  
Qy 399 ATCATGCTTTTGTAGTGATACAGTGGATTAACGCCGTTGGATTCTCTCTCCATTCGG 458  
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Db 826 TTTTGTATACATATTTGCACACACCCCATCTCTCACTCCCTCATATATGATTCACACCGAAT 885  
Qy 939 GGAATCGATCAAAAGGCGCTTATCAACAAATCGATAGGATTTCCGGTTCCTGAAATCGG 998  
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RESULT 5
AY166773 LOCUS              1419 bp      mRNA      linear      PLN 02-JUN-2003
DEFINITION Helianthus annuus delta12-fatty acid acetylase mRNA, complete
               cds.
ACCESSION  AY166773
VERSION     AY166773.1 GI:31322134
KEYWORDS   Helianthus annuus (common sunflower)
SOURCE     Helianthus annuus
ORGANISM   Helianthus annuus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Helianthus.
REFERENCE   1 (bases 1 to 1419)
            Cahoon,E.B., Schnurr,J.A., Huffman,E.A. and Minto,R.E.
            Fungal responsive fatty acid acetylases occur widely in
            evolutionarily distant plant families
JOURNAL    Plant J. 34 (5), 671-683 (2003)
AUTHORS    Cahoon,E.B.
TITLE      Direct Submission
JOURNAL    Submitted (18-OCT-2002) Crop Genetics, DuPont, Bldg. 402
            Experimental Station, Wilmington, DE 19880-0402, USA
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                        /db_xref="GI:31322135"
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ORIGIN
Query Match      47.3%; Score 664.8; DB 4; Length 1419;
Best Local Similarity 76.4%; Pred. No. 4.1e-150;
Matches 845; Conservative 0; Mismatches 252; Indels 9; Gaps 2;

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Qy      189 CAATCCCTGCATTTGTTCCGGCGATCCCGCGTCTGGTCACTCTGCTAGCTAGTTGTTCCAGG 248
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Qy      249 ATCTCATTTATCACCTTCTCTTTATACAGCGTGCACACACCTACATCTTCCCTCACCTCCCTC 308
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Qy      309 CTCCTCTAGTTTACTTAGCATGCGCGGTTTACTCGGTTTGCCAACTTTGCAATCTTGCACTCTCACTG 368
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.

1 (bases 1 to 1312)

Stymne, S., Green, A., Singh, S. and Lenman, M.  
Plant fatty acid epoxigenase genes and uses therefor  
Patent: JP 2001518797-A 2 16-OCT-2001;  
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN  
STYMNE

COMMENT

OS Crepis sp.  
PN JP 2001518797-A/2  
PD 16-OCT-2001  
PP 09-APR-1998 JP 1998543302  
PR 15-APR-1997 AU PO 6223.15-APR-1997 AU PO 6226 PR  
16-APR-1997 US 60/043706, 20-JUN-1997 US 60/050403 PI STEN  
STYMNE, ALIAN GREEN, SURINDER SINGH, MARIT LENMAN PC  
C12N15/53, C12N9/02  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT CDS 26..1147.

FEATURES

source

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Query Match 46.8%; Score 657.6; DB 2; Length 1312;  
Best Local Similarity 76.4%; Pred. No. 2.2e-148;  
Matches 836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGGATTTGATCCGGCGCATCTTCGTTAACTGATGATTAAGAAAGCAATCCCT 196  
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QY 137 GCACATTCGTTCCGGGATCCGGCTCTGGTCATCTCTAGTGTTCAGATCTCATT 256  
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DB 311 ATCCTCGGCCATGAATGTGGTCAACATGCCCTATAGCAACTACATGGGTTGACACACT 370  
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QY 497 CGAAAGCAACATGCAACACAAATTCATCTGAAAGAGGAGGATTTACCTCTAGAACT 556  
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DB 1085 AGGAAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1138  
QY 1217 CATAAATGTAATC 1230  
DB 1139 CATAAATGTAATC 1152

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DEFINITION Sequence 3 from patent US 6329518.  
ACCESSION AR367438  
VERSION AR367438.1 GI:34600637  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1312)  
AUTHORS Green, A., Singh, S., Lenman, M. and Stymne, S.  
TITLE Plant fatty acid epoxigenase genes and uses therefor  
JOURNAL Patent: US 6329518-A 3 11-DEC-2001;  
BASF Plant Science GmbH and Commonwealth Scientific & Industrial  
Research Organisation; Ludwigshafen;  
DEX;

FEATURES

source

1..1312 Location/Qualifiers  
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ORIGIN

Query Match 46.8%; Score 657.6; DB 2; Length 1312;  
Best Local Similarity 76.4%; Pred. No. 2.2e-148;  
Matches 836; Conservative 0; Mismatches 246; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGGATTTGATCCGGCGCATCTTCGTTAACTGATGATTAAGAAAGCAATCCCT 196  
DB 71 GAACGTTCTCAGTTGATCCAGTAACTTCTCACTGAGTGATTTGAAGCAAGCAATCCCT 130  
QY 197 GCACATTCGTTCCGGGATCCGGCTCTGGTCATCTCTAGTGTTCAGATCTCATT 256  
DB 131 CCACATTCGTTCCAGCGATGTGTATCGGTTTCATCTTATTACGTTGTTGAGATCTCATA 190  
QY 257 ATCACTTCCTTTTATACAGCGTCCGCAACACTACATTCCTCACTCCCTCCTCTCTA 316







|                       |  |  |                                    |
|-----------------------|--|--|------------------------------------|
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| QY                    | 1082   | GCATCAAGCCACTCTTGGGTGATTACAGGATGATCGACAGGACTCCATTTTCAAAGCA         | 1141                               |
| Db                    | 895  | GCATCATACCACTTTTGGGTGAATTTTATAAGATCGATAGGACTCCATCTTTAAAGCA         | 954                                |
| QY                    | 1142   | ATGTGAGAGAGGCCAAGGAATGC  | 1165                               |
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| ACCESSION             | BD061164   |  |                                    |
| VERSION               | BD061164.1   | GI:22606770  |                                    |
| KEYWORDS              | JP 2001518797-A/1.   |  |                                    |
| SOURCE                | Zea mays   |  |                                    |
| ORGANISM              | Zea mays   |  |                                    |
| REFERENCE             |  |  |                                    |
| AUTHORS               | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |  |                                    |
| TITLE                 | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  |  |                                    |
| JOURNAL               | clade; Panicoideae; Andropogoneae; Zea.                            |  |                                    |
|                       | 1 (bases 1 to 1358)  |  |                                    |
|                       | Stymne, S., Green, A., Singh, S. and Lenman, M.                    |  |                                    |
|                       | Plant fatty acid epoxigenase genes and uses therefor               |  |                                    |
|                       | Patent: JP 2001518797-A 1 16-OCT-2001;                             |  |                                    |
|                       | COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN |  |                                    |
| COMMENT               | STYMNE   |  |                                    |
|                       | PN JP 2001518797-A/1   |  |                                    |
|                       | PD 16-OCT-2001   |  |                                    |
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|                       | PR 15-APR-1997 AU PO 6223,15-APR-1997 AU PO 6226 PR                |  |                                    |
|                       | 16-APR-1997 US 60/043706,20-JUN-1997 US 60/050403 PI STEN          |  |                                    |
|                       | STYMNE, ALLAN GREEN, SURINDER SINGH, MARIT LENMAN PC               |  |                                    |
|                       | C12N15/53, C12N9/02  |  |                                    |
|                       | CC Strandedness: Single;   |  |                                    |
|                       | CC Topology: Linear;   |  |                                    |
|                       | FH Key Location/Qualifiers   |  |                                    |
|                       | FT CDS 30..1151.   |  |                                    |
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| ORIGIN                |  |  |                                    |
| Query Match           | 45.5%;   | Score 640.4;   | DB 2; Length 1358;                 |
| Best Local Similarity | 75.5%;   | Pred. No. 3.4e-144;  |                                    |
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| QY                    | 137  | GAACGAGCCCGATTGATCGCGGCCATCTCTGTTAAGTGCATTAAGAAAGCAATCCCT          | 196                                |
| Db                    | 75   | GAACGTGCTCAGTTGATCCAGTAACTCTCTCACTGAGTGAATGAAGCAAGCAATCCCT         | 134                                |
| QY                    | 197  | GCACATTGCTTCGGCGGATCCGCGCTCTGCTCATCTCTGCTACGTCAGTTCAGGATCTCAT      | 256                                |
| Db                    | 135  | CCCCATTGCTTCAGAGATCTGTAATCCGCTCATCTACTAATGTTGTTCAAGATCTCAT         | 194                                |
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| Db                    | 195  | ATTGCGCTACATCTTCTACTCTCTTGGCAACACATATATCCCTACTCTCTCTACTAGTCTA      | 254                                |
| QY                    | 317  | GTTTACTTACGATCGCGGTTTACTGTTTGGCAATCTTGCATCTCTCACTGTTTATGG          | 376                                |
| Db                    | 255  | GCTTACTTACTTGGGCGGTTTACTGTTTCTGTCAAGCTAGCGTCTCTCACTGGCTTATGG       | 314                                |
| QY                    | 377  | GTCTCTCGGCATGAATGCGGCCATCATGCTTTAGTGAGTACAGTGGATTGTATACGCC         | 436                                |
| Db                    | 315  | ATCTCTCGGCACGAATGTGTCACCAATGCTTTAGCACTACATCATGTTTACGACACT          | 374                                |
| QY                    | 437  | GTTGGAATTCGTCTCCATTCGGCTCTCTCACCCCTTACTTTTCTTTGGAAATACAGCCAT       | 496                                |
| Db                    |  |  |                                    |
| Db                    | 375  | GTGGGCTTCATCTCCACTCATTTCTCTCAACCCCGATTTCTCTTGGAAATTCAGTCAC         | 434                                |
| QY                    | 497  | CGAAAGCACCATGCAAAACACAAATTCACTCGAAACAGAGAAAGTTTACATTTCTTAGAACT     | 556                                |
| Db                    | 435  | CGAATCACCATTCCACACAAAGTTTCGATTGATACGATGAAGTTTACATTTCCGAAAGC        | 494                                |
| QY                    | 557  | CAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTTGACAAACGCTGTGTCGAATC        | 616                                |
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| QY                    | 617  | CTCATCTTGTTCATCATGTTTAACTTAGGATTTCTTTATACCTCTTACGATGTTTCA          | 676                                |
| Db                    | 549  | TTGGTTTTGATTTATCATGTTTCACCTTAGGATTTCTTTATACCTCTTGAACAATATTTCC      | 608                                |
| QY                    | 677  | GGCAAGAAGTCAGATAGATTACCAACCACTTTTGATCCATTGAGCCCGATCTTCCACGAG       | 736                                |
| Db                    | 609  | GGCAAGAATACGACAGGTTTGGCAACCACTTCGACCCCATGAGTCCATTTTCAAGAA          | 668                                |
| QY                    | 737  | CGTGAGCGAATCCAGTTCGGTTTATCAGATCTTTGGTATCGTTGCGAGTGTTTACGGAATC      | 796                                |
| Db                    | 669  | CGTGAGCGGTTTTCAGGCTCTTCTTTGGATCTTTGGTCTTCTTGGCGGTGTTTATGGAAT       | 728                                |
| QY                    | 797  | AGTTTCTTGTGACAAACAAAGGATTTGGTTCGGTATGTCATGTCATGTCAGTTCAGTTC        | 856                                |
| Db                    | 729  | AAAGTTCGTGTAGCAAAATAAGGAGCTGCTTGGTAGCGTGCATGTCATGTCGCGTA           | 788                                |
| QY                    | 857  | ATAGGTCTGAATTCCTTCATTTATCGTAATCACTTATCTGCACCAACACATCTGTCTCA        | 916                                |
| Db                    | 789  | TTAGGCGTATTTACCTTTTTCGATGTGATCACCTTCTTGCACCAACACCATCAGTCTCG        | 848                                |
| QY                    | 917  | CCCCATTAGATTCACCGAATGGAACCTGGATCAAGAGGACCTTGACCAACATTCGACAGA       | 976                                |
| Db                    | 849  | CCTCATTTATGATCAACTGAATGGAACCTGGATCAGAGGGGCTTGTGACCAATTCGATAG       | 908                                |
| QY                    | 977  | GATTTCCGCTCTCGAATCGGGTTTTCACAGAGCTTACACACACCCACCTGTGACCAT          | 1036                               |
| Db                    | 909  | GACTTTGGATTCCTGAATAGTGTGTTTCCATGATGTTTACACACTCATGTCATGTCATCAT      | 968                                |
| QY                    | 1037   | TTGTTTCCCTACATTCACATTTATCATGTAATCACTTATCTGCACCAACACATCTGTCTCA      | 1096                               |
| Db                    | 969  | TTGTTTTCATATTTCCACACTATCATGCAAGAGGCAAGGAGGACCAATCAAGCCAAATC        | 1028                               |
| QY                    | 1097   | TTGGGTGATTCAGGATGATCGACGAGCTTCATTTTCAAAGCAATGTGGAGAGAGGCC          | 1156                               |
| Db                    | 1029   | TTGGGCGACTTTTATATGATCGACAGGACTCCAAATTTTAAAGCAATGTGGAGAGAGGCC       | 1088                               |
| QY                    | 1157   | AAGGAATGCATTTACATCGAGCAAGATGACAGCAAGCAACAGGACATATTTGGTAC           | 1216                               |
| Db                    | 1089   | AGGGAGTGCATGTACATCGAGC-----CTGATAGCAAGCTCAAAGGTGTTTATTGGTAT        | 1142                               |
| QY                    | 1217   | CATAAAATGTAATC   | 1230                               |
| Db                    | 1143   | CATAAATGTGATC  | 1156                               |
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| LOCUS                 | CS023935   | 1358 bp  | DNA linear PAT 03-MAR-2005         |
| DEFINITION            | Sequence 3 from Patent WO2005014831.                               |  |                                    |
| ACCESSION             | CS023935   |  |                                    |
| VERSION               | CS023935.1   | GI:60495624  |                                    |
| KEYWORDS              | Crepis palaestina  |  |                                    |
| SOURCE                | Crepis palaestina  |  |                                    |
| ORGANISM              | Crepis palaestina  |  |                                    |
| REFERENCE             |  |  |                                    |
| AUTHORS               | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |  |                                    |
| TITLE                 | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; |  |                                    |
| JOURNAL               | asterids; campanulids; Asterales; Asteraceae; Cichorioideae;       |  |                                    |
|                       | Cichorieae; Crepis.  |  |                                    |
|                       | 1  |  |                                    |
|                       | Poirier, Y., Rezzonico, E. and Moire, L.                           |  |                                    |
|                       | Fatty acid biosynthesis 2  |  |                                    |
|                       | Patent: WO 2005014831-A 3 17-FEB-2005;                             |  |                                    |
|                       | The University of York (GB)  |  |                                    |

|                       |  |  |                                    |
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| Db                    | 969                                      | TTGTTTTTCAATATTCACATATCATGCAAGGAGGCAAGGATGCAATCAAGCAATC        | 1021                               |
| QY                    | 1097                                     | TTGGGTGATTTACAGGATGATCGACAGGACTCCATTTTTTCAAAGCAATGTGGAGAGAGCC  | 1156                               |
| Db                    | 1029                                     | TTGGGGGACTTTTATATGATCGACAGGACTCCAAATTTTAAAGCAATGTGGAGAGAGGC    | 1088                               |
| QY                    | 1157                                     | AAGGAATGCATTTTACATCGAGCAAGATCGACAGCAGCAAGGAGGACATATTTGGTAC     | 1216                               |
| Db                    | 1089                                     | AGGGAGTGCATGTACATCGAGC-----CTGATAGCAAGCTCAAAGGTGTTTATTGGTAT    | 1142                               |
| QY                    | 1217                                     | CATATAATGTAATC   | 1230                               |
| Db                    | 1143                                     | CATAAATGTGATC  | 1156                               |
| RESULT 12             |  |  |                                    |
| LOCUS                 | CS023951                                 | Sequence 3 from Patent WO2005014833.                           |                                    |
| DEFINITION            | CS023951                                 | 1358 bp  | DNA                                |
| ACCESSION             | CS023951                                 |  | linear                             |
| VERSION               | CS023951.1                               | GI:60495634  | PAT 03-MAR-2005                    |
| KEYWORDS              |  |  |                                    |
| SOURCE                | Crepis palaeolina                        |  |                                    |
| ORGANISM              | Crepis palaeolina                        |  |                                    |
| REFERENCE             |  |  |                                    |
| AUTHORS               | Poirier, Y., Rezzonico, E. and Moire, L. |  |                                    |
| TITLE                 | Fatty acid biosynthesis 1                |  |                                    |
| JOURNAL               | Patent: WO 2005014833-A 3 17-FEB-2005;   |  |                                    |
| FEATURES              | The University of York (GB)              |  |                                    |
| source                | Location/Qualifiers                      |  |                                    |
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|                       | /db_xref="taxon:72611"                   |  |                                    |
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| Best Local Similarity | 75.5%;                                   | Pred. No. 3.4e-144;  |                                    |
| Matches               | 826;                                     | Conservative 0;  | Mismatches 256; Indels 12; Gaps 2; |
| QY                    | 137                                      | GAACGAGCCCGATTTGATCCGCGCCATTCCTCGTTAAAGTGAATCAAGAAAGCAATCCCT   | 196                                |
| Db                    | 75                                       | GAACGTGTCTCAGTTGATCCAGATCTGTAATCCGCTCATCTTACTATGTTTCAAGATCTCAT | 134                                |
| QY                    | 197                                      | GCACATTTGCTTCGCGCGATCCGCGCTCTGTCATCTCTGCTAGTATTCAGGATCTCAT     | 256                                |
| Db                    | 135                                      | CCCCATTTGCTTCCAGAGATCTGTAATCCGCTCATCTTACTATGTTTCAAGATCTCAT     | 194                                |
| QY                    | 257                                      | ATCACCTTCTTTTATACACGGTTCGCCAACACCTACATTCCTCACCTCCTCCTCTA       | 316                                |
| Db                    | 195                                      | ATTGCTTACATCTTCTACTTCTTCCCAACACATATATCCCTACTCTTCTACTAGTCTA     | 254                                |
| QY                    | 317                                      | GTTTACTTAGCATGCGCGTTTACTGGTTTTCGCCAATCTTGCACTCTCCTGTTTATGG     | 376                                |
| Db                    | 255                                      | GCCTACTTAGCTTGGCGGTTTACTGGTTTCTGCAAGCTAGCTCCTCCTCCTCTA         | 314                                |
| QY                    | 377                                      | GTCTCTCGGCGATGAATCGCGCCATCATGCTTTTAGTGAGTACCAGTGGATTGATACGCC   | 436                                |
| Db                    | 315                                      | ATCTCGGCCACGAATGTGTCACCATGCTTTAGCAACTACACATGTTTGGACGACT        | 374                                |
| QY                    | 437                                      | GTTGGATTTGCTTCCCATTCGGCTCTCCTCACCCCTTACTTTTCTTGGAAATACAGCCAT   | 496                                |
| Db                    | 375                                      | GTTGGCTTCATCTCCACTCATTTCTCTCACCCGTTATTTCTTGGAAATTCAGTCCAC      | 434                                |
| QY                    | 497                                      | CGAAAGCACCATGCAACACAAATTCATCTCGAAACGAGGAGTTTACATTCCTAGAACT     | 556                                |
| Db                    | 435                                      | CGGAATCACCATTCGAACCAAGTTTCGATGTAACGATGAAGTTTACATTCGGAAGC       | 494                                |
| QY                    | 557                                      | CAGTCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACACACGCTGGTCGATC       | 616                                |
| Db                    | 495                                      | AAGTCCAAACTCGCGGT-----ATCTATAAATCTTTTAAACACCCACTGGTCGGCTG      | 548                                |
| QY                    | 617                                      | CTCATCTTGGTCATCATGTTTAACTTAGGATTTCTTTTATACCTCTTAAACGAATGTTCA   | 676                                |
| Db                    | 549                                      | TTGGTTTGAATATCATGTTTCACTTAGGATTTCTTTTATACCTCTTGAACAATATTTCC    | 608                                |
| QY                    | 677                                      | GGCAAGAGTACGATAGATTTTACCAACCACTTTGATCCATTTGAGCCCGATCTTCCCGAG   | 736                                |
| Db                    | 609                                      | GGCAAGAAATACGACAGGTTTGGCAACCACTTCGACCCCAATGAGTCCAAATTTCAAAGAA  | 668                                |
| QY                    | 737                                      | CGTGAGCGAATCCAGGTTGGTTATCAGATCTTGGTATCGTTTGGCAGTGTTTTACGGACTC  | 796                                |
| Db                    | 669                                      | CGTGAGCGGTTTACAGTCTTCTTCCGATCTTGGTCTTCTTGGCGGTGTTTATGGAAT      | 728                                |
| QY                    | 797                                      | AAGTTTCTTGACAAACAAAGGATTTGGTTGGGTGATGTGATGATGAGTTTCCAGTG       | 856                                |
| Db                    | 729                                      | AAAGTTGCTGTAGCAATAAAGGAGCTGCTTGGGTAGCGTGTGATGATGAGTTTCCGTA     | 788                                |
| QY                    | 857                                      | ATAGGCTGTAATTCCTTCAATATCGTAATCACTTATCTGCACCAACACATCTGTGCTCA    | 916                                |
| Db                    | 789                                      | TTAGCGGATTTTACTTTTTCGATGATCACTTCTTTCGACCAACCAATCAGTCTGTG       | 848                                |
| QY                    | 917                                      | CCCCATTACGATTCACCGAATGAACTGGATTCAAAGAGGCGTTTGACCAACATCGACAGA   | 976                                |
| Db                    | 849                                      | CCTCATTTATGATTCAACTGAAATGAACTGGATCAGAGGGGCTTGTGAGCAATCGATAGG   | 908                                |
| QY                    | 977                                      | GATTTCCGCTCTCGTAATCGGGTTTTCCAGAGCTTACACACCCCAAGTGTGCAACAT      | 1036                               |
| Db                    | 909                                      | GACTTTGGATTTCTGAAATAGTGTGTTTTCATGATGTTTACACACATCATGTATGATCAT   | 968                                |
| QY                    | 1037                                     | TTGTTTCTCCTACATTTCCACATTTATCATGCAAGAGGAGGCAAGGCGCATCAAGCCCAATC | 1096                               |

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LOCUS CS023971 1358 bp DNA linear PAT 03-MAR-2005
DEFINITION Sequence 5 from Patent WO2005014834.
ACCESSION CS023971
VERSION CS023971.1 GI:60495648
KEYWORDS
SOURCE
ORGANISM
Crepis palaestina
Crepis palaestina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Crepis.
1
REFERENCE
1. 1358
AUTHORS
Renz, A.
TITLE
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JOURNAL
Patent: WO 2005014834-A 5 17-FEB-2005;
The University of York (GB)
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Location/Qualifiers
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Query Match 45.5%; Score 640.4; DB 2; Length 1358;
Best Local Similarity 75.5%; Pred. No. 3.4e-144;
Matches 826; Conservative 0; Mismatches 154; Indels 12; Gaps 2;

QY 137 GAACGAGCCCGGATTTGATTCGGCGCCATTTCTCGTTAACTGATCTAAAGAAAGCAATCCCT 196
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QY 197 GCACATTTGCTTCGGCGGATTCGGCGTCTGCTGATCTCTCTAGTAGTACGATCTCAAT 256
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QY 257 ATCACTTCTCTTTTATACACGGTTCGCAACCACTTACATTTCTCACTCCCTCTCTCTCTA 316
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DB 609 GCGAAGAAATACGACAGGTTTGGCCAACTTTCGACCCCATGAGTCCAAATTTTCAAGAA 668
QY 737 CGTAGCGAATCCAGGTTGCGTTTATCAGATCTTGTGATGCTTGTGAGTGTGTTTACGAGTCT 796
DB 669 CGTAGCGGTTTTCAGGCTCTCTTTTCGGATCTTGGTCTTCTTGGCCGTGTTTATGGAAT 728
QY 797 AAGTTTCTTTACAAACAAAGGATTTGGTGGGTGATGTGATGATGATGGATTTCCAGTG 856
DB 729 AAGTTGCTGTAGCAATTAAGAGAGCTGCTTGGGTAGCGTGATGTATGGAGTTCGGTA 788
QY 857 ATAGTCTGAAATCTCTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATG 916
DB 789 TTAGGCGTATTTTACCTTTTTCGGATCTTGGTCTTCTTGGCCGTGTTTATGGAAT 848
QY 917 CCCAATTACGATTTCAACCGAATGGAATCTGGATCAAGAGGCTTGCACCACTTCCACAGA 976
DB 849 CCTCATTTATGATTTCACTGATGGAATGGAATCTGATGAGAGGGCTTGTGACCAATCGATAG 908
QY 977 GATTTTCGGTCTCTGAAATCGGTTTTTCCACGAGTTCACACAGGCTTACACAGGCTGTTGACCAT 1036
DB 909 GACTTTGGATTTCTGAAATAGTGTGTTTTCATGATGTTTACACACATCTCATGTGATGATCAT 968
QY 1037 TTGTTTCCCTACATTTCCACATTTATCATGCAAGAGGCAAGAGGCCATCAAGCCAATC 1096
DB 969 TTGTTTTCATATTTCCACACTATCATGCAAGAGGCAAGGATGCAATCAAGCCAATC 1028
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DB 1143 CATAAATGTGATC 1156
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Db 1089 AGGAGTGCATGTACATCGAGC-----CTGATAGCAAGCTCAAAAGGTGTTTATTGGTAT 1142
Qy 1217 CATAAATGTAATC 1230
Db 1143 CATAAATTGTGATC 1156

RESULT 14
LOCUS AR367437 1358 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 1 from patent US 6329518.
ACCESSION AR367437
VERSION AR367437.1 GI:34600636
KEYWORDS Unknwn.
SOURCE Unknwn.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1358)
AUTHORS Green,A., Singh,S., Lenman,M. and Stymne,S.
TITLE Plant fatty acid epoxigenase genes and uses therefor
JOURNAL Patent: US 6329518-A 1 11-DEC-2001;
BASF Plant Science GmbH and Commonwealth Scientific & Industrial
Research Organisation; Ludwigshafen;
DEX,
FEATURES Location/Qualifiers
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Query Match 45.5%; Score 640.4; DB 2; Length 1358;
Best Local Similarity 75.5%; Pred. No. 3.4e-144;
Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;
Qy 137 GAACGAGCCCGATGTATCCGGCGCATCTCTGGTTAAGTGATCTAAAGAAAGCAATCCCT 196
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1143 CATAAATTGTGATC 1156

RESULT 15
LOCUS AX031160 1358 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 1 from Patent WO9846762.
ACCESSION AX031160
VERSION AX031160.1 GI:10278513
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Green,A., Singh,S., Stymne,S. and Lenman,M.
TITLE Plant fatty acid epoxigenase genes and uses therefor
JOURNAL Patent: WO 9846762-A 1 22-OCT-1998;
GREEN ALLAN (AU) ; SINGH SURINDER (AU) ; COMMW SCIENT IND RES ORG
(AU) ; STYMNE SPEN (SE) ; LENMAN MARIT (SE)
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CDS
ORIGIN
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| QY | 1157 | AAGGATCGATTTACATCGAGCAAGATCGACAGCAAGGACATATTTGGTAC        | 1211 |
| Db | 1089 | AGGGAGTCCATGTACATCGAGC-----CTGATAGCAAGCTCAAGAGTGTATTGGTAT | 1142 |
| QY | 1217 | CATATAAATGTAATC   | 1230 |
| Db | 1143 | CATATAAATGTGATC   | 1156 |

Search completed: September 25, 2006, 00:56:11

Job time : 8120 secs

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